

241 CCAGACTTCGGGCGGAGCGCCCTCCGCGGCTCCGGAGCCGCGGTGAGCCCTGCGGGCCAT 300
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481 GCACTGAGGCTTCGCGACCCGAGAACACTTCCTGCTGCTCAACCTCGACCTTCGCACTT 540
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BD235872 2699 bp DNA linear PART 17-JUL-2003
LOCUS Isolated DNA encoding human H3 histamine receptor.
DEFINITION BD235872
ACCESSION BD235872.1 GI:33045642
VERSION JP 2002526049-A/5.
KEYWORDS
SOURCE synthetic construct
ORGANISM
other sequences; artificial sequences.
1 (bases 1 to 2699)
Labenberg, T.W., Erlander, M., Huber, A. and Piatel, J.
Isolated DNA encoding human H3 histamine receptor
Patent: JP 2002526049-A 5 20-AUG-2002;
ORTHO MCNEIL PHARMACEUTICAL INC
COMMENT
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PN JP 2002526049-A/5
PD 20-AUG-2002
PF 07-OCT-1998 JP 2000573370
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PIATEL
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Location/Qualifiers
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DB 1 CAACGCTCCGCGCGTGCACGGTGCACCGGACGGGCTCAGGCTCCGGCTCTCTCC 60
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|
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DB 61 GTTGACAGACCGCGCTGCGCGCCCACTGGGCTCGGATCCGGCCCCCGCTTCGCA 120
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|
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DB 181 ACCGACCCGCGCAAGGGCCCGCAAGAAGAGGCTCCGGGCGCGGCGCCCTCCGCGCG 240
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DB 241 CCCAGCTCTCGGCGCGGCGCCCTCCGCGCTCCCGAGCGCGGTAGCCTGGGGGCGAT 300
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DB 1141 CGTAGGCGGTGAAGCGCGGAGAGCGACCTTCGAGGAGTGGCGGTGCGGCTCGGTGCG 1200
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|
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QY 1261 GAGGGGCTCAAGCGGTGCGGCTCTCGGCTGAGAGAGCGCATGAAGAGGTGTC 1320
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|
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Db	1261	GAGGGGCTCCAAAGCCGTGGGGGTCTCTGGGCTCTCGTGGAGAAAGGCAATGAAGATGATGTC	1320
Oy	1321	CCAGAAGCTTCAACCCAGCCCTTTCCGCTGTCTCGGGACAGAAAGTGGCCAAAGTCGTGGC	1380
Db	1321	CCAGAGCTTCAACCCAGCCCTTTCCGCTGTCTCGGGACAGAAAGTGGCCAAAGTGGTCGGC	1380
Oy	1381	GGTAACTGTAGACACTTTGGGCTCTGTGGGGCCCCCAACAGCGCTGATGATCATCCG	1440
Db	1381	GGTAACTGTAGACACTTTGGGCTCTGTGGGGCCCCCAACAGCGCTGATGATCATCCG	1440
Oy	1441	GGCCGCTCGCCATGGCCCACTGCGTCCCTGACTACTGTATACGAAACTCTCTCTGGCTCT	1500
Db	1441	GGCCGCTCGCCATGGCCCACTGCGTCCCTGACTACTGTATACGAAACTCTCTCTGGCTCT	1500
Oy	1501	GTGGGCAACTCTGGCTGTCAACCCCTGTCTCTACCTCTGTGGCCACCAAGCTTCCGCG	1560
Db	1501	GTGGGCAACTCTGGCTGTCAACCCCTGTCTCTACCTCTGTGGCCACCAAGCTTCCGCG	1560
Oy	1561	GGCCCTTCAACAAGCTGTCTGGCCCCCAGAAAGTCCAAATCCAGCCCCCAGCTCCGTGG	1620
Db	1561	GGCCCTTCAACAAGCTGTCTGGCCCCCAGAAAGTCCAAATCCAGCCCCCAGCTCCGTGG	1620
Oy	1621	GCACCTGTGAAGTGAAGTGGGCCCAACAGAGCTTCCTTCAGCCAGCCCTCTCTCAGCCAG	1680
Db	1621	GCACCTGTGAAGTGAAGTGGGCCCAACAGAGCTTCCTTCAGCCAGCCCTCTCTCAGCCAG	1680
Oy	1681	GTCTCTGGGCAATCTGGCCCTGTGCCCCCTTAACCCGAGCTCGTCCCTCCAGGGGTGAGCC	1740
Db	1681	GTCTCTGGGCAATCTGGCCCTGTGCCCCCTTAACCCGAGCTCGTCCCTCCAGGGGTGAGCC	1740
Oy	1741	CGCGCTGTCTGGGCTCTCTCTTAATGCAAGGAGCCACCTCGCAATGAGAGGGGCTTC	1800
Db	1741	CGCGCTGTCTGGGCTCTCTCTTAATGCAAGGAGCCACCTCGCAATGAGAGGGGCTTC	1800
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Db	1801	CTGGGTTGGCCAGAGGGCCCTCTCACTGGCTGGAAGGAGGCTGGGTGGCCGGCCCTGCC	1860
Oy	1861	CCCACTTTCTGCTTCCACCGGGAGAGGACAGTCTGAGAGTCCAGACATGCTGCCACC	1920
Db	1861	CCCACTTTCTGCTTCCACCGGGAGAGGACAGTCTGAGAGTCCAGACATGCTGCCACC	1920
Oy	1921	CGTGTGGTGGCCACCCTTGGCAGTTACTGTGGTGTCTTCCCAAGCAAGACCTGG	1980
Db	1921	CGTGTGGTGGCCACCCTTGGCAGTTACTGTGGTGTCTTCCCAAGCAAGACCTGG	1980
Oy	1981	GTGTGCTCCAGGCTTCTGACCCTAGACAGTTTGGCTCTGACGTGACACACCTGCAACC	2040
Db	1981	GTGTGCTCCAGGCTTCTGACCCTAGACAGTTTGGCTCTGACGTGACACACCTGCAACC	2040
Oy	2041	CTGTGACACCTGTGACACCGTCTCCCTCCCGAACAAGCCAGAGACACTGCTTGTG	2100
Db	2041	CTGTGACACACCTGTGACACCGTCTCCCTCCCGAACAAGCCAGAGACACTGCTTGTG	2100
Oy	2101	CGTCTGTCTCTGTGATAGCTCTAGAGCTGAGCCCTTCAACCCCTTCCCAACAACCT	2160
Db	2101	CGTCTGTCTCTGTGATAGCTCTAGAGCTGAGCCCTTCAACCCCTTCCCAACAACCT	2160
Oy	2161	CTGTGCCCCCAAAAGTGTCAAGGGGCCCTTGAAGACCTGGAAGCTGTTCTGTCTTTTCCA	2220
Db	2161	CTGTGCCCCCAAAAGTGTCAAGGGGCCCTTGAAGACCTGGAAGCTGTTCTGTCTTTTCCA	2220
Oy	2221	TTCTGGGTGTTTTAGAAAGATGAAGAAACAATGTCTGTGAACCTTGATGTTGTGTGG	2280
Db	2221	TTCTGGGTGTTTTAGAAAGATGAAGAAACAATGTCTGTGAACCTTGATGTTGTGTGG	2280
Oy	2281	ATGTTTAATCAAGAGACAAATTTGCTGAAGAGCTCAGGCTGGAATTTGCAAGTGTGGG	2340
Db	2281	ATGTTTAATCAAGAGACAAATTTGCTGAAGAGCTCAGGCTGGAATTTGCAAGTGTGGG	2340
Oy	2341	CTCCACAGCCCTCTCCCTCGCTAAGGCTTCCGCTGAGGTGTCAGAGCTTCTGGC	2400
Db	2341	CTCCACAGCCCTCTCCCTCGCTAAGGCTTCCGCTGAGGTGTCAGAGCTTCTGGC	2400

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Db	421	GGCGCTGCTCATCGTGGCCACGGTCTGGGCAACGCGCTGGTCATGCTCGCTTGTTGGC	480
QY	481	CGACTCGAGCCCTCGGCAACCTTCTTCTGCTCAACCTCGGCATCTCCGACTT	540
Db	481	CGACTCGAGCCCTCGGCAACCTTCTTCTGCTCAACCTCGGCATCTCCGACTT	540
QY	541	CCTCGTCGGCGCTCTGTGATCCCACTGTATGTACCTTACGTGTGACAGGCGCGCTGGAC	600
Db	541	CCTCGTCGGCGCTCTGTGATCCCACTGTATGTACCTTACGTGTGACAGGCGCGCTGGAC	600
QY	601	CTTGGGCGGGGCGCTGTGCAAGCTGTGGCTGGTAGTGAATCACTGTGTGACCTCTCTC	660
Db	601	CTTGGGCGGGGCGCTGTGCAAGCTGTGGCTGGTAGTGAATCACTGTGTGACCTCTCTC	660
QY	661	TGCGTTCAACATCGGTCTATCAGTTAGACCGCTTCTGTGCGGACCGGAGCGGTCTC	720
Db	661	TGCGTTCAACATCGGTCTATCAGTTAGACCGCTTCTGTGCGGACCGGAGCGGTCTC	720
QY	721	ATACCGGGGCCAGCAGGGGTGACACGCGCGGGGACAGTGGGAAAGATGTGCTGTGGGT	780
Db	721	ATACCGGGGCCAGCAGGGGTGACACGCGCGGGGACAGTGGGAAAGATGTGCTGTGGGT	780
QY	781	GCTGGCGCTTCTGTCTGTACGGAACGACGCCATCTGTAGCTGGAGTACCTGTCCGGGGGAG	840
Db	781	GCTGGCGCTTCTGTCTGTACGGAACGACGCCATCTGTAGCTGGAGTACCTGTCCGGGGGAG	840
QY	841	CTCCATCCCCGAGGGGCACTGTGTATGCCAGATTCTTTCAACACTGGTACTTCTCATAC	900
Db	841	CTCCATCCCCGAGGGGCACTGTGTATGCCAGATTCTTTCAACACTGGTACTTCTCATAC	900
QY	901	GGCTTCAACCCGAGAGTCTTTTAGGCCCTTCTCAAGGCTCACTTTAACTCAAGAT	960
Db	901	GGCTTCAACCCGAGAGTCTTTTAGGCCCTTCTCAAGGCTCACTTTAACTCAAGAT	960
QY	961	CTACTGTGAATCCAGAGGCGCACCGGCTCGGCTGTGATGGGGCTCGAGAGGACCGG	1020
Db	961	CTACTGTGAATCCAGAGGCGCACCGGCTCGGCTGTGATGGGGCTCGAGAGGACCGG	1020
QY	1021	CCCGAGCCCCCTCCGAGGGCCGAGCCCTCAACACCCCAACCGGCTGTGGGGCTG	1080
Db	1021	CCCGAGCCCCCTCCGAGGGCCGAGCCCTCAACACCCCAACCGGCTGTGGGGCTG	1080
QY	1081	CTGGCAGAAAGGGGCAACGGGGAGCCATCCGCTGTGACAGGTATGGGGTGGGTGAGGCGGC	1140
Db	1081	CTGGCAGAAAGGGGCAACGGGGAGCCATCCGCTGTGACAGGTATGGGGTGGGTGAGGCGGC	1140
QY	1141	CGTAGGCGCTGAGGCGGGGAGGCGACCTCGGGGGTGGCGGTGGGGCGGCTCGTGGC	1200
Db	1141	CGTAGGCGCTGAGGCGGGGAGGCGACCTCGGGGGTGGCGGTGGGGCGGCTCGTGGC	1200
QY	1201	TTCAACCACTTCAGCTCCGCGACGCTCTCTGAGAGGGCACTGAGAGGCCGCGCTCACTCAA	1260
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QY	1261	GAGGGGCTTCGAAGCGGTGGGGTCTCTCGGCTCTGTCGAGAAAGGCAATGAATGTGTCTC	1320
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QY	1321	CGAGAGCTTCAACCGAGCGCTTTCGGCTGTCTCGGGACAGGAAAGTGGCGAAGTGGCGGC	1380
Db	1321	CGAGAGCTTCAACCGAGCGCTTTCGGCTGTCTCGGGACAGGAAAGTGGCGAAGTGGCGGC	1380
QY	1381	CGTATCGTAGAGCATTTTGGGCTGTGCTGGGCCCAACACGCTGCTGATGATATCCG	1440
Db	1381	CGTATCGTAGAGCATTTTGGGCTGTGCTGGGCCCAACACGCTGCTGATGATATCCG	1440
QY	1441	GGCGCGCTGCAATGGGCACTGCGTCTCTGACTACTGTGTACGAAACCTCTTCTGGCTCT	1500
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[illegible]

Df	2581	GTGACCCCGTGCAGCGCCTCTGCATGCTCTTCGTGGCTGGCTGGCTGCCCTGCA	26400
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DEFINITION	Sequence 548 from Patent WO02061087.		
ACCESSION	AX549263		
VERSION	AX549263.1	GI:25813942	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE			
AUTHORS	Burner,G.C., Roush,C.L. and Brown,J.P.		
TITLE	Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides		
JOURNAL	Patent: WO 02061087-A 548 08-MUG-2002;		
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Query Match	100.0%; Score 2699; DB 6; Length 2699;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 2699; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
OY	1	CCAAGCGTCCGCGGCTGTGACGGTGTGACCCGGACGGGCTGAAGCTCCGCTCTCCC	60
Df	1	CCACCCTGCGCGCGGCTGCACGGTGTGACCCGGACGGGCTGAAGCTCCGCTCTCCC	60
OY	61	GCTGAGAGAGCGGCGCTGCGCGGCCCCCACTGGGGCTGGATCGGGCCCCCGGCGCA	120
Df	61	GCTGAGAGAGCGGCGCTGCGCGGCCCCCACTGGGGCTGGATCGGGCCCCCGGCGCA	120
OY	121	CGCGCTGTGTGCGCCCGCGCGCGCGCGCGCGCATGCGCTGGCGCGCCCCGAGAGA	180
Df	121	CGCGCTGTGTGCGCCCGCGCGCGCGCGCGCGCATGCGCTGGCGCGCCCCGAGAGA	180
OY	181	ACCGAACCGGCGAAGGGCGCGAAGACGAGAGCTCCGGGCGGGGCGCTCCCGGCGG	240
Df	181	ACCGAACCGGCGAAGGGCGCGAAGACGAGAGCTCCGGGCGGGGCGCTCCCGGCGG	240
OY	241	CCGAGCTCTGGGCGGGGCGCGCGCGCGCGCGCGCGAGCGCGGTGAGCGTGGGGGCAT	300
Df	241	CCGAGCTCTGGGCGGGGCGCGCGCGCGCGCGCGCGAGCGCGGTGAGCGTGGGGGCAT	300
OY	301	GAGCG	360
Df	301	GAGCG	360
OY	361	GAGCG	420
Df	361	GAGCG	420
OY	421	GAGCG	480
Df	421	GAGCG	480
OY	481	GAGCTCGAGCTCGCACCGACCAATTCTTCTGCTCAACCTCGGCATCTCGACTT	540
Df	481	GAGCTCGAGCTCGCACCGACCAATTCTTCTGCTCAACCTCGGCATCTCGACTT	540

QY	541	CCTGTGGGGGCGCTTTGCAATCCACGTGATGATACCTGATGCTGTA	CAGGCGCGTGGAC	600
.Db	541	CCTGTGGGGGCGCTTTGCAATCCACGTGATGATACCTGATGCTGTA	CAGGCGCGTGGAC	600
QY	601	CTTGGGCGCGGGGGCGCTTGGACGCTGTGGCTGGATGAGACTACCTGCTGGACCTTC	660	
Db	601	CTTGGGCGCGGGGGCGCTTGGACGCTGTGGCTGGATGAGACTACCTGCTGGACCTTC	660	
QY	661	TGCTTCAACATCGTGCTCATCAGCTACGACCGCTTCTGTGCGGTACCCGAGCGGTCTC	720	
Db	661	TGCTTCAACATCGTGCTCATCAGCTACGACCGCTTCTGTGCGGTACCCGAGCGGTCTC	720	
QY	721	ATACCGGGGCGCAGGAGGGGTGACAGGGGGCGGGGACGTGGAGAAATGCGCTGGGTGGGT	780	
Db	721	ATACCGGGGCGCAGGAGGGGTGACAGGGGGCGGGGACGTGGAGAAATGCTGGGTGGGT	780	
QY	781	GCTGGCGCTTCCGTGTATACGAGACCAAGCCATCTTACGTGGAGATACCTGTCCGGGGCAG	840	
Db	781	GCTGGCGCTTCCGTGTATACGAGACCAAGCCATCTTACGTGGAGATACCTGTCCGGGGCAG	840	
QY	841	CTCCATCCCGGAGGGCCACTGTCTATGCGGAGTTCTTCAACATGATATCTTCTCATAC	900	
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QY	901	GCGTTTCAACCCGTGAGTTCTTATGAGCCCTTCAGGGTCACTTCTTTAACCCTACAT	960	
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Db	961	CTACCTGAACATCCAGAGGCGCACCCGCGCTCCGCTGATGAGGGCTGAGAGGACGCGG	1020	
QY	1021	CCCGGAGCCCCCTCCGAGGCGCCAGCCCTCACACCCCCACCGCTGAGCTGTGGGCTG	1080	
Db	1021	CCCGGAGCCCCCTCCGAGGCGCCAGCCCTCACACCCCCACCGCTGAGCTGTGGGCTG	1080	
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Db	1081	CTGGCAGAAAGGGGCGACGGGGAGGCGCATGCGCTGCACAGATATGGGGTGGGTAGGGCGG	1140	
QY	1141	CGTAGGCGCTGAGGCGGGGAGGCGACCCCTGCGGGGTGGCGTGGGGGCGGCTCCGTGGC	1200	
Db	1141	CGTAGGCGCTGAGGCGGGGAGGCGACCCCTGCGGGGTGGCGTGGGGGCGGCTCCGTGGC	1200	
QY	1201	TTCAACCACTCCAGCTCCGGCAGCTCCTCGAGGGGCGCTGAGAGGCGCGCGCTCATCAA	1260	
Db	1201	TTCAACCACTCCAGCTCCGGCAGCTCCTCGAGGGGCGCTGAGAGGCGCGCGCTCATCAA	1260	
QY	1261	GAGGGGCGCTCAAGCGCGTGGCGCTTGGGCTCTGCTGAGAAAGGCGATGAAAGTGGTGT	1320	
Db	1261	GAGGGGCGCTCAAGCGCGTGGCGCTTGGGCTCTGCTGAGAAAGGCGATGAAAGTGGTGT	1320	
QY	1321	CGAGAGCTTCAACCCAGCGCTTCCGCTGTCTCGGGAAGGAAATGGACCAAGTGCCTGGC	1380	
Db	1321	CGAGAGCTTCAACCCAGCGCTTCCGCTGTCTCGGGAAGGAAATGGACCAAGTGCCTGGC	1380	
QY	1381	CGTCACTGTGAGCATCTTGGGACTCTGTGGGCGCCATACCGCTGTGATGATCATCG	1440	
Db	1381	CGTCACTGTGAGCATCTTGGGACTCTGTGGGCGCCATACCGCTGTGATGATCATCG	1440	
QY	1441	GCGCGCGCTGCAATGGCCACTGCGCTGCCGTGACTATGTGATAGMAAACCTTCCTTGGGCTCT	1500	
Db	1441	GCGCGCGCTGCAATGGCCACTGCGCTGCCGTGACTATGTGATAGMAAACCTTCCTTGGGCTCT	1500	
QY	1501	GTTGGGCCAATCGGCTGTCAACCTGTGCTCTACCTGTGGGACCAACAGCTTCCGCGG	1560	
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QY	1561	GCGCTTCAACCAAGCTGCTTGGCGCCCGGAGAGCTCAAAATCCAGGCCCAAGCTTCCCTGA	1620	
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QY	1621	GCACTGTGAGATGATGGGCCCAACAGAGCTTCCCTAGCACGCTTCTTACGCCAG	1680	

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AF140538
LOCUS AF140538 2699 bp mRNA linear PRI 10-JUN-1999
DEFINITION Homo sapiens histamine H3 receptor mRNA, complete cds.
ACCESSION AF140538
VERSION AF140538.1 GI:5031290
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Lovenberg, T.W., Roland, B.L., Wilson, S.J., Jiang, X., Pyati, J.,
Huvar, A., Jackson, M.R. and Erlander, M.E.
TITLE Cloning and functional expression of the human histamine H3
receptor.
JOURNAL Mol. Pharmacol. 55 (6), 1101-1107 (1999)
MEDLINE 99278519
PUBMED 10347254
AUTHORS Lovenberg, T.W., Roland, B.R., Wilson, S.J., Jiang, X., Pyati, J.,
Huvar, A., Jackson, M.R. and Erlander, M.E.
TITLE Direct Submission
JOURNAL Submitted (05-Apr-1999) Molecular Pharmacology, RW Johnson PRI,
3535 General Atomics Ct, San Diego, CA 92121, USA
FEATURES
source 1..2699
/organism="Homo sapiens"
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299..1636
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/translation="MERAPDGPDLNAGSLADGADAAAGARGFSAWTAVALMALNLI
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ORIGIN

Query Match 100.0%; Score 2699; DB 9; Length 2699;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES	JOURNAL	source
LOCUS	AR104201	
DEFINITION	Sequence 1 from patent US 6093545.	DNA linear PAT 14-FEB-2001
ACCESSION	AR104201	
VERSION	AR104201.1	GI:12816909
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 2689)	
AUTHORS	Goodearl, A.D.J. and Glucksmann, M. Alexandra.	
TITLE	Methods for detecting nucleic acid molecules encoding a member of the muscarinic family of receptors	
JOURNAL	Patent: US 6093545-A 1 25-0UL-2000;	
FEATURES	Location/Qualifiers	
source	1..2689	

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QY	85 CCACTGGGCTTGATCCGGCCCCCGCCCCCTTCGGACCGCTGCTCTGGCCCCCG	144		
Db	78 CCACTGGGCTTGATCCGGCCCCCGCCCCCTTCGGACCGCTGCTCTGGCCCCCG	137		
QY	145 GCCCCGAGGACCATATCGCTGGGCGCCCCCAGAGGAAACCGACCCGGGCGAGGCGCGCA	204		
Db	138 GCCCCGAGGACCATATCGCTGGGCGCCCCCAGAGGAGAACCGACCCGGGCGAGGCGCGCA	196		
QY	205 AAGAAGAGGCTCCCGGCGCGGGGCCCTTCCCGCCGCGCCAGCTTTCGCGCGGCGCTTGC	264		
Db	197 AAGAAGAGGCTCCCGGCGCGGGGCCCTTCCCGCCGCGCCAGCTTTCGCGCGGCGCTTGC	256		
QY	265 CCCGCGTCCGGAAGCGCGCTGAGGCTGGGGGACCATGAGGCGCGCGCGCGCGAGCGGGCC	324		
Db	257 CCCGCGTCCGGAAGCGCGCTGAGGCTGGGGGACCATGAGGCGCGCGCGCGCGAGCGGGCC	316		
QY	325 GCTGAAAGCTTCGGGAGGCGCTTGGCGGCGGATGCGGCGGCGCGGCGGGGCGCGCGCTT	384		
Db	317 GCTGAAAGCTTCGGGAGGCGCTTGGCGGCGGATGCGGCGGCGCGGCGGGGCGCGCGCTT	376		
QY	385 CTGGGAGCCGTGAGCCGCGGATGCTGGCGCGGCTCATATGGCGGTGCTCATATGGGCGACGCT	444		
Db	377 CTGGGAGCCGTGAGCCGCGGATGCTGGCGCGGCTCATATGGCGGTGCTCATATGGGCGACGCT	436		
QY	445 GCTGGGAGCGCGCTGATCATGCTTCGCTTGTGGCGGACTCGAGCCTCGGACCCAGAA	504		
Db	437 GCTGGGAGCGCGCTGATCATGCTTGTGGCGGACTCGAGCCTCGGACCCAGAA	496		
QY	505 CAACCTTCTTCGTCGACCTCGGACCTCGGACCTTCGTCGCGGCGCTTCGACATCC	564		
Db	497 CAACCTTCTTCGTCGACCTCGGACCTTCGTCGCGGCGCTTCGACATCC	556		
QY	565 ACTGTATATACCTTACGCTGACAGCGCGCTGGACTTTCGGCGGGGCGCTTCGACAGCT	624		

Db	557	ACTGATATBACCCATACGATCGTGAACAGGCGGTGAGACCTTGGCCGCGGAGCCTCTGCAAGCT	616
Qy	625	GTGCGTGTAGTGAAGTAACCTGCTGTGTGCACTCTCTGTGCTTTCAACATCGTGCATCAG	684
Db	617	GTGGCGGTGTAGTGAAGTACTCGTGTGTGCACTCTCTGTGCTTTCAACATCGTGCATCAG	676
Qy	685	CTAGACCGGCTTCCGTGCGGTCAACCGGAGGGGTCTATACCGGGGCCAGCGGGTGAAC	744
Db	677	CTACGACCGGCTTCCGTGCGGTCAACCGGAGGGGTCTATACCGGGGCCAGCGGGTGAAC	736
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Qy	805	AGCCATCTTGAAGTGGAGTACTGTCTCGGGGGGAGCTCATCCCGAGGGCCACTGTCTA	864
Db	797	AGCCATCTTGAAGTGGAGTACTGTCTCGGGGGGAGCTCATCCCGAGGGCCACTGTCTA	856
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DB 2056 CTCTCCCGGACAGCCGACGACCTGTGCTTGTGCTTGTCTTGTCAATTAAGCTC 2115
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DB 2476 GTTGGGAGAGAGGGGCGCGGCTGTGGGCTCGAAGGCTGTGAGAGGGGCTGTGAGA 2535
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LOCUS BD086285 2689 bp DNA linear part 27-AUG-2002

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DEFINITION G protein-coupled receptor and utilization thereof.
ACCESSION BD086285
VERSION BD086285.1 GI:22631895
KEYWORDS JP 2001525174-A/1.
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2689)
AUTHORS Goodearl,A.D.J., Glucksmann,A.M., Xie,M. and Distefano,P.
TITLE G protein-coupled receptor and utilization thereof
JOURNAL Patent: JP 2001525174-A 11-DEC-2001;
MILLENNIUM PHARMACEUTICALS INC
COMMENT
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PN JP 2001525174-A/1
PD 11-DEC-2001
PE 04-DEC-1998 JP 2000523346
PR 04-DEC-1997 US 08/985090 17-MAR-1998 US 09/042780 PT
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DISTEFANO
PC C12N15/09, C07K14/705, C07K16/28, C12N5/10, C12P21/02, C12Q1/68//
CC (C12P21/02, C12R1:91), C12N15/00, C12N5/00
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CC Topology: linear;
CC G protein-coupled receptor and utilization thereof FH key
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Query Match 97.6%; Score 2635.2; DB 6; Length 2689;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
OY 25 GCGACGGGACGCGCTCAGGCTCCGGCTCTCTCCGGTGCAGACAGCGCGTGCAGCC 84
DB 18 CGACCGGACGCGCTCAGGCTCCGGCTCTCTCCGGTGCAGACAGCGCGTGCAGCC 77
OY 85 CCACCTGGGCTGGATCCGCGCCCGGCTCCGCTCGGACCGGCTGTGTGGCCCGGCGCC 144
DB 78 CCACCTGGGCTGGATCCGCGCCCGGCTCCGCTCGGACCGGCTGTGTGGCCCGGCGCC 137
OY 145 GCGCGCGGACCATGCGCTGGAGCGCGCCCGGAGGAAACCGGACCGGCGCAAGGAGCCGCA 204
DB 138 GCGCGCGGACCATGCGCTGGAGCGCGCCCGGAGGAGGAAACCGGACCGGCGCAAGGAGCCGCA 196
OY 205 AAGACGAGGCTCCCGGAGCGCGGAGCCCTCCGCGCGCGCCAGCTCTGGCCGCGCTTGC 264
DB 197 AAGACGAGGCTCCCGGAGCGCGGAGCCCTCCGCGCGCGCCAGCTCTGGCCGCGCTTGC 256
OY 265 CCGCGTCTCCGAGACCGCGTGTGAGCTGTGGGAGCATGAGAGCGCGCGCCCGGAGCGCC 324
DB 257 CCGCGTCTCCGAGACCGCGTGTGAGCTGTGGGAGCATGAGAGCGCGCGCCCGGAGCGCC 316
OY 325 GCTGAACCTTCGAGGAGCGGTGAGCGGAGATGCGGAGCGGAGCGGAGCGGAGCGGCTT 384
DB 317 GCTGAACCTTCGAGGAGCGGTGAGCGGAGATGCGGAGCGGAGCGGAGCGGAGCGGCTT 376
OY 385 CTGGGACACCTGAGACCGCGGTGTGGCGCGCTCAATGAGCGGTCTCATGTGGCCAGGT 444
DB 377 CTGGGACACCTGAGACCGCGGTGTGGCGCGCTCAATGAGCGGTCTCATGTGGCCAGGT 436
OY 445 GCTGGGCAACCGCGGTGTGATGCTGTGCTTGTGTGGCGCATGTGAGCGGTCTCCGACCA 504
DB 437 GCTGGGCAACCGCGGTGTGATGCTGTGCTTGTGTGGCGCATGTGAGCGGTCTCCGACCA 496
OY 505 CAACCTTCTTCGCTCAACCTGACATCTCGACCTTCTCGCGGCGGCTTCTGTGATCC 564
DB 497 CAACCTTCTTCGCTCAACCTGACATCTCGACCTTCTCGCGGCGGCTTCTGTGATCC 556

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OY	565	ACTGATATGTAACCTTAACGTGTGACACAGAGCCGCTGTGACACTTTGGCCGGGGCCCTCTGCAACT	624
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OY	625	GTGACTGGTAAGTGAATACTCTGTGTGACACTCTCTGTGCTTCAACATCTGTCTATGAG	684
Db	617	GTGACTGGTAAGTGAATACTCTGTGTGACACTCTCTGTGCTTCAACATCTGTCTATGAG	676
OY	665	CTACGACCGCTTCTGTGTGCTCACTCCGAGCGGTCTCATACGGGGCCACGAGGTGACAC	744
Db	677	CTACGACCGCTTCTGTGTGCTCACTCCGAGCGGTCTCATACGGGGCCACGAGGTGACAC	736
OY	745	GGGGGGGGGACAGTGGGGAAGATGCTGTGTGTGGGTGTGGCTTCTGTGTGTGATGAGAC	804
Db	737	GGGGGGGGGACAGTGGGGAAGATGCTGTGTGTGGGTGTGGCTTCTGTGTGTGATGAGAC	796
OY	805	AGCCATCTCTGAGCTGGAGTACTCTGTCCGGGGGACAGCTCAATCCCGAGGGGCACTGTGTA	864
Db	797	AGCCATCTCTGAGCTGGAGTACTCTGTCCGGGGGACAGCTCAATCCCGAGGGGCACTGTGTA	856
OY	865	TGCCAGATTCTTCTAACACTGTGTACTTCTCTCATCAAGGCTTTCACCCCTGAGATTCTTTAC	924
Db	857	TGCCAGATTCTTCTAACACTGTGTACTTCTCTCTCATCAAGGCTTTCACCCCTGAGATTCTTTAC	916
OY	925	GCCCTTCTCTAGCGTCACTCTTTTAACCTCAAGCATCTAACATCTCAGAGGCGCAC	984
Db	917	GCCCTTCTCTAGCGTCACTCTTTTAACCTCAAGCATCTAACATCTCAGAGGCGCAC	976
OY	985	CCGACTCTCCGGCTGGAATGGGGGCTCCAGAGGACCGGCCCCGAGGCCCTCCCGAGGGCCA	1044
Db	977	CCGACTCTCCGGCTGGAATGGGGGCTCCAGAGGACCGGCCCCGAGGCCCTCCCGAGGGCCA	1036
OY	1045	GCCCTCACCAACCCCAACCGCCTGTGTCTGTGGGCTGTGTGGAGAGAGGGGACAGGGGAGGC	1104
Db	1037	GCCCTCACCAACCCCAACCGCCTGTGTGTGGGCTGTGTGGAGAGAGGGGACAGGGGAGGC	1096
OY	1105	CATGCGCTGCAACAGGTATGTGGGTGTGGTGAAGCGGCGCTGAGCGCTGAGGCGGGAGAGC	1164
Db	1097	CATGCGCTGCAACAGGTATGTGGGTGTGGTGAAGCGGCGCTGAGGCGGTGAGGCGGGAGAGC	1156
OY	1165	GACCCTCGGGGGTGGCGGGTGGGGGGGGGCGCTCGGTGGCTTCAACCAACTCTCCAGCTCCGAG	1224
Db	1157	GACCCTCGGGGGTGGCGGGTGGGGGGGGGCGCTCGGTGGCTTCAACCAACTCTCCGAG	1216
OY	1225	CTCCTCGAGGGGCACTGAGAGGCGCGCTCACTCAAGAGGGGCTTCAAGCGGTGGCGCTC	1284
Db	1217	CTCCTCGAGGGGCACTGAGAGGCGCGCTCACTCAAGAGGGGCTTCAAGCGGTGGCGCTC	1276
OY	1285	CTCGGCGCTGTGCGAGGAACGCGATGAGATGATGTGTCCAGAGCTTACCCAGCGCTTTCG	1344
Db	1277	CTCGGCGCTGTGCGAGGAACGCGATGAGATGATGTGTCCAGAGCTTACCCAGCGCTTTCG	1336
OY	1345	GCTGTCTGTGGGACAGGGAAGTGGGCCAATCGCTGTGGCGCTCAATCGTGAACATCTTTGGGCT	1404
Db	1337	GCTGTCTGTGGGACAGGGAAGTGGCCAATCGCTGTGGCGCTCAATCGTGAACATCTTTGGGCT	1396
OY	1405	CTGTGTGGGCGCCCATYACAGCTGTGTGATGATCACTCGGGGCGGCTGTGACACTGTGGT	1464
Db	1397	CTGTGTGGGCGCCCATYACAGCTGTGTGATGATCACTCGGGGCGGCTGTGACACTGTGGT	1456
OY	1465	CCCTGACTACTGTGACGAACCTCTCTTGTGGCTCTGTGTGGGCAAACTGTGCTGTCAACC	1524
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OY	1525	TGTCTCTTAACCTCTGTGTGACCAACAGCTTTCGCGGGGCTTCAACAAAGCTGTCTGTGCC	1584
Db	1517	TGTCTCTTAACCTCTGTGTGACCAACAGCTTTCGCGGGGCTTCAACAAAGCTGTCTGTGCC	1576
OY	1585	CCAGAAAGTCAAAAATCCAGAGCCCAACAGCTCTCTGTGAGCACTGTGTGAAGTGAAGTGGCCCA	1644
Db	1577	CCAGAAAGTCAAAAATCCAGAGCCCAACAGCTCTCTGTGAGCACTGTGTGAAGTGAAGTGGCCCA	1636
OY	1645	CCAGAGCTCCCTCTAGCCAGCGCTTCTCTAGAGCCAGGCTTCTGTGGGACATCTGAGCGCTT	1704

Db	1637	CGAAGCCTCCCTAGCACGCTCTCTCAGCCAGATCTCTGGACATCTGGACCTGCT	1696
QY	1705	GCCCCCTACCGGCTCTGTTCCCCCAAGGGTGAACCCCGCGTGTCTGTGGCCCTCTTTA	1764
Db	1697	GCCCCCTACCGGCTGCTTCCCCCAAGGGTGAACCCCGCGTGTCTGTGGCCCTCTTTA	1756
QY	1765	ATGCCACGGACGCCACTCTGCCATGAGAGGCGCTTCTGTGGTGTGGCCAGAGGCCCTCTCA	1824
Db	1757	ATGCCACGGACGCCACTCTGCCATGAGAGGCGCTTCTGTGGTGTGGCCAGAGGCCCTCTCA	1816
QY	1825	CTGGCTGGACATGAGAGGCTGGGTGGCGGCGCTGGCCGCCCAATTGCTGGCTCAACGGGGGA	1884
Db	1817	CTGGCTGGACTGAGAGGCTGGGTGGCGGCGCTGGCCGCCCAATTGCTGGCTCAACGGGGGA	1875
QY	1885	GGGACAGCTCTGAGAGTCCAGAGATGCTGGCCACCCCTGTGTGGTCCACACCTTGGAG	1944
Db	1876	GGGACAGCTCTGAGAGTCCAGAGATGCTGGCCACCCCTGTGTGGTCCACACCTTGGAG	1935
QY	1945	TTACTGATGATGTCTTCTCCCAAGAGACACTGGGTGTGCTCCAGGCTTCTGACCTTA	2004
Db	1936	TTACTGATGATGTCTTCTCCCAAGAGAGACTGGGTGTGCTCCAGGCTTCTGACCTTA	1995
QY	2005	GCAATTTGCTCTGTGCACATGACACACCTGTGCACACCCCTGTGCACACACCTGTGC	2064
Db	1996	GCAATTTGCTCTGTGCACATGACACACCTGTGCACACCCCTGTGCACACACCTGTGC	2055
QY	2065	CTCTCCCCGAGCAAGCCAGAGACATGAGCTTGTGCTGCTCTGTGCTTGTGCAAGGCTC	2124
Db	2056	CTCTCCCCGAGCAAGCCAGAGACATGAGCTTGTGCTGCTCTGTGCTTGTGCAAGGCTC	2115
QY	2125	AGGCGCTGACCTTTCACCCCTCTTCCCAACCACTCTCTGTGCCCCCAAAAGTGTCAAGG	2184
Db	2116	AGGCGCTGACCTTTCACCCCTCTTCCCAACCACTCTCTGTGCCCCCAAAAGTGTCAAGG	2175
QY	2185	GCCCTAGGAACCTTCGAAGCTGTTCTCTGCTTTTCCATTGTGGGTGTTTCAAGAAAGTGA	2244
Db	2176	GCCCTAGGAACCTTCGAAGCTGTTCTCTGCTTTTCCATTGTGGGTGTTTCAAGAAAGTGA	2235
QY	2245	AGAGAAATCAATGCTGTGTGAACCTTGAATGTTGCGGGATGTTTAATCAAGAGAGCAAAAT	2304
Db	2236	AGAGAAATCAATGCTGTGTGAACCTTGAATGTTTCTGGGATGTTTAATCAAGAGAGCAAAAT	2295
QY	2305	TGCTGAGAGACTCAGGACTGTGATTTGGCAGGTGTGGCTCCACGCGCTTCTCCCTCGCT	2364
Db	2296	TGCTGAGAGACTCAGGACTGTGATTTGGCAGGTGTGGCTCCACGCGCTTCTCCCTCGCT	2355
QY	2365	AAGGCTTCCGGCTGAGCTGTGTGCAAGCTGTCTTGCCACCCCGCTCTGTGGCTCACACCA	2424
Db	2356	AAGGCTTCCGGCTGAGCTGTGTGCAAGCTGTCTTGCCACCCCGCTCTGTGGCTCACACCA	2415
QY	2425	GCCCTGTGTGCAAGGCTGCGCCCGGCACTGTTTGTGCTCAACCGAGGACTCTGGGGGTT	2484
Db	2416	GCCCTGTGTGCAAGGCTGCGCCCGGCACTGTTTGTGCTCAACCGAGGACTCTGGGGGTT	2475
QY	2485	GTTGGAGAGAGGGAGCCCGGCTGTGGGCCGACAGGGTCCCAAGAGGCTGCAAGGGCGGTCCAGA	2544
Db	2476	GTTGGAGAGAGGGAGCCCGGCTGTGGGCCGACAGGGTCCCAAGAGGCTGCAAGGGCGGTCCAGA	2535
QY	2545	GGAAGTCCCGGCAAGGGGCGGCTTGGCATGTGCTGTGCACCCGTTGCCACGCGCTTGC	2604
Db	2536	GGAAGTCCCGGCAAGGGGCGGCTTGGCATGTGCTGTGCACCCGTTGCCACGCGCTTGC	2595
QY	2605	ATGCTCTCTGTGCTGTGCCCCGCTGTGCTGCTCCCTTGCAAAACCGTAGAGTCACAATAAAGTGT	2664
Db	2596	ATGCTCTCTGTGCTGTGCCCCGCTGTGCTGCTCCCTTGCAAAACCGTAGAGTCACAATAAAGTGT	2655
QY	2665	ATTTTTTTAAAAAATTTTTTTTTT	2688
Db	2656	ATTTTTTTAAAAAATTTTTTTTTT	2679

RESULT 8


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Db      1743 TGTGGCCCTCTCTTAATGCGACGGCAGACCCTGCGCATGAGAGCGCTTCTGAGTTGG 1802
Oy      1810 CCAGAGGGGCCCTCATTTGGCTGGAATGAGAGCTGGGTGGCCGGCCCTTGCCCCCAATTC 1869
Db      1803 CCAGAGGGGCCCTCATTTGGCTGGAATGAGAGCTGGGTGGCCGGCCCTTGCCCCCAATTC 1862
Oy      1870 TGGCTTCACCGGAGGAGGACAGTCTGAGAGTCCCAACATGCTGCCCCCCTGCTGGT 1929
Db      1863 TGGCTTCACCGGAGGAGGACAGTCTGAGAGTCCCAACATGCTGCCCCCCTGCTGGT 1921
Oy      1930 GCCACACCTTTCGAGTACTGTTGGTGTCTTCCAAAGACAGACCTGGGTGGCTCC 1989
Db      1922 GCCACACCTTTCGAGTACTGTTGGTGTCTTCCAAAGACAGACCTGGGTGGCTCC 1981
Oy      1990 AGGCTTCCCTGCTAGACATTTGCTCTGACGTGACACACCTGACACCCCTGACAC 2049
Db      1982 AGGCTTCCCTGCTAGACATTTGCTCTGACGTGACACACCTGACACCCCTGACAC 2041
Oy      2050 ACTGACACACCGTCCCTGCCCCGAGACAGGCCAGGACATGCTTGTGCTGCTGTC 2109
Db      2042 ACTGACACACCGTCCCTGCCCCGAGACAGGCCAGGACATGCTTGTGCTGCTGTC 2101
Oy      2110 TCTTGCATTAAGCTCTAGGCTGAGCTTTCACCCCTCTTCCCACTCTCTGCCCC 2169
Db      2102 TCTTGCATTAAGCTCTAGGCTGAGCTTTCACCCCTCTTCCCACTCTCTGCCCC 2161
Oy      2170 CAAAAGTGCAGAGGGGCCCTTAGAAGCTGTAAGCTGTTCTCTGCTTTTTCATTCTGGG 2229
Db      2162 CAAAAGTGCAGAGGGGCCCTTAGAAGCTGTAAGCTGTTCTCTGCTTTTTCATTCTGGG 2221
Oy      2230 TTTTTCAGAAAGATGAAGAAAGAAACATGCTGTGAACTTGATGTTGTGGAGATTTAAT 2289
Db      2222 TTTTTCAGAAAGATGAAGAAAGAAACATGCTGTGAACTTGATGTTGTGGAGATTTAAT 2281
Oy      2290 CAAAGAGAGCAAAATTTGCTGAGAGGCTCAAGGCTGATTTGGCAGTGTGGCTCCACGC 2349
Db      2282 CAAAGAGAGCAAAATTTGCTGAGAGGCTCAAGGCTGATTTGGCAGTGTGGCTCCACGC 2341
Oy      2350 CCTCTCTCCTCCGCTAAGGCTTCCGCTGAGCTGTGAGCTGCTCTTCTGCCCCCCTG 2409
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Oy      2410 TCTGGGCTCAACACGACCCCTGCTGGGCGCAGGCCGCGCCCACTCTGTTTGTGACCCA 2469
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Oy      2470 GGACCTCTGGGGGTTTGTGGAGAGAGGGGCGCGCTGGGCGCAGAGGATCCAAAGCGTG 2529
Db      2462 GGACCTCTGGGGGTTTGTGGAGAGAGGGGCGCGCTGGGCGCAGAGGATCCAAAGCGTG 2521
Oy      2530 CAGGGGCGGTTCCAGAGAGAGGTGCGCGGCGCAGGGCGCTTGGCATGTGCTGTGACACCG 2589
Db      2522 CAGGGGCGGTTCCAGAGAGAGGTGCGCGGCGCAGGGCGCTTGGCATGTGCTGTGACACCG 2581
Oy      2590 TGGCAGCGGCTCGAGATGCTCTCTGCTGCTGCTGCGCGCTGCGCTGCGCAACCGTGAG 2649
Db      2582 TGGCAGCGGCTCGAGATGCTCTCTGCTGCTGCTGCGCGCTGCGCTGCGCAACCGTGAG 2641
Oy      2650 GTCAACATAAAGTGTATTTTTTTA 2673
Db      2642 GTCAACATAAAGTGTATTTTTTTA 2665

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RESULT 9
LOCUS    HS1005F21
DEFINITION
          HS1005F21 100976 bp DNA linear PRI 24-APR-2001
          Human DNA sequence from clone RP5-1005F21 on chromosome 20. Contains
          the PSMA7 gene for proteasome subunit 7, alpha type (prosome,
          macropain), the HRH3 gene encoding histamine receptor H3, the
          KIAA0693 gene similar to SSXT (synovial sarcoma, translocated to X
          chromosome), a novel gene for a GTP-binding protein, the 3' end of
          a novel gene similar to Pleurodeles waltlil RAP55 protein, 7 Cpg
          islands, ESTs, STSs and GSSE, complete sequence.

```

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ACCESSION AL078633
VERSION    AL078633.32
KEYWORDS   HTG: CCG island; GTP-binding protein; histamine receptor; HRH3;
          KIAA0693; macropain; PSMA7; prosome; proteasome; SSXT; synovial
          sarcoma.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 100976)
          Corby, N.
          Direct Submission
          Submitted (24-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
          CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
          requests: clonerequest@sanger.ac.uk
          On Jul 23, 2000 this sequence version replaced gi:8919366.
          During sequence assembly data is compared from overlapping clones.
          Where differences are found these are annotated as variations
          together with a note of the overlapping clone name. Note that the
          variation annotation may not be found in the sequence submission
          corresponding to the overlapping clone, as we submit sequences with
          only a small overlap as described above.
          The following abbreviations are used to associate primary accession
          numbers given in the feature table with their source databases:
          Bm: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormBase; Information
          from the WORMPEP database can be found at
          http://www.sanger.ac.uk/Projects/C_elegans/wormpep
          This sequence was generated from part of bacterial clone contigs of human
          chromosome 20, constructed by the Sanger Centre Chromosome 20
          Mapping Group. Further information can be found at
          http://www.sanger.ac.uk/HGP/Chr20
          This sequence is the entire insert of clone RP5-1005F21. The true
          left end of clone RP11-11M20 is at 81766 in this sequence. The true
          right end of clone RP11-157P1 is at 51899 in this sequence. This
          sequence was finished as follows unless otherwise noted: all
          regions were either double-stranded or sequenced with an alternate
          chemistry or covered by high quality data (i.e., phred quality >=
          30); an attempt was made to resolve all sequencing problems, such
          as compressions and repeats; all regions were covered by at least
          one plasmid subclone or more than one M13 subclone; and the
          assembly was confirmed by restriction digest. RP5-1005F21 is from
          the library RPCT-5 constructed by the group of Pieter de Jong. For
          further details see
          http://www.chori.org/bacpac/home.htm
          VECTOR: pCYPAC2.
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     repeat_region    1671..1927
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     repeat_region    3036..3149
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repeat_region 5274..5675 /note="201 copies 2 mer tg 59% conserved"
repeat_region 5292..5675 /note="12 copies 32 mer 63% conserved"
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repeat_region 5341..5439 /note="3 copies 33 mer 96% conserved"
repeat_region 5349..5543 /note="5 copies 39 mer 65% conserved"
repeat_region 5386..5931 /note="26 copies 21 mer 54% conserved"
repeat_region 5407..5678 /note="8 copies 34 mer 66% conserved"
repeat_region 5440..5538 /note="3 copies 33 mer 79% conserved"
repeat_region 5502..5669 /note="7 copies 24 mer 69% conserved"
repeat_region 5507..5676 /note="17 copies 10 mer gtcgtgtgtc 69% conserved"
repeat_region 5509..5676 /note="12 copies 14 mer 69% conserved"
repeat_region 5640..5787 /note="4 copies 37 mer 77% conserved"
repeat_region 5658..5789 /note="4 copies 33 mer 72% conserved"
repeat_region 5760..5825 /note="33 copies 2 mer gt 71% conserved"
repeat_region 5801..6163 /note="11 copies 33 mer 62% conserved"
repeat_region 5879..5980 /note="3 copies 34 mer 79% conserved"
repeat_region 5931..6176 /note="3 copies 82 mer 72% conserved"
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repeat_region 6130..6199 /note="5 copies 14 mer 75% conserved"
repeat_region 6229..6376 /note="4 copies 37 mer 69% conserved"
repeat_region 6333..6652 /note="10 copies 32 mer 67% conserved"
repeat_region 6353..6454 /note="3 copies 34 mer 80% conserved"
repeat_region 6414..6602 /note="9 copies 21 mer 65% conserved"
repeat_region 6423..6492 /note="7 copies 10 mer gggagtgtgt 77% conserved"
repeat_region 6425..6498 /note="37 copies 2 mer gt 74% conserved"
repeat_region 6480..6631 /note="8 copies 19 mer 73% conserved"
repeat_region 6483..6652 /note="5 copies 34 mer 75% conserved"
repeat_region 6852..6903 /note="26 copies 2 mer ca 75% conserved"
repeat_region 6909..6992 /note="6 copies 14 mer 72% conserved"
repeat_region 6910..6989 /note="40 copies 2 mer ac 67% conserved"
repeat_region 7464..7555 /note="46 copies 2 mer gg 62% conserved"
repeat_region 9023..9155 /note="FLAM_C repeat: matches 1..133 of consensus"
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repeat_region 14429..14472 /note="22 copies 2 mer tg 75% conserved"
misc_feature 14611..16552 /note="CpG island"
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repeat_region 15295..15384 /note="14 copies 9 mer gggggggggc 61% conserved"
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/evidence=not_experimental

Query Match 72.2%; Score 1949.4; DB 9; Length 100976;
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Matches 1973; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

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QY 739 TGACACGCGCGCGGACGTCGGAAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 798
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DB 18833 CGGACCAAGCATCTGAGCTGGAGTACTGTCTCGGGGGGAGCTCATCTCCGAGGGCCA 18892
QY 859 CTGCTATGCCGAGTCTTCTCAACTGGAATCTCTCATACGGGTTCCACCTCGAGATT 918
DB 18893 CTGCTATGCCGAGTCTTCTCAACTGGAATCTCTCATACGGGTTCCACCTCGAGATT 18952
QY 919 CTTTACGCCCTTCTCAGCGTACCTCTTTTAACTTCAGCATCTTCAATCCAGACAGAG 978
DB 18953 CTTTACGCCCTTCTCAGCGTACCTCTTTTAACTTCAGCATCTTCAATCCAGACAGAG 19012
QY 979 GCGACCCGCTCGGCTGAGATGGGCTCGAGAGGACCGGCGCCCGGACCCCTTCCCGA 1038
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Db	19073	GGCCAGCCCTCAACAACCCCAACCGCTTGCTGTGGGCTGTGACAGAGGACAG	19132
Qy	1099	GGAGGCCATGCGCTGCAACAGGTATGGGGTGGGTAGCGGGCCGTAGGCGCTGAGGCCGG	1158
Db	19133	GGAGGCCATGCGCTGCAACAGGTATGGGGTGGGTAGCGGGCCGTAGGCGCTGAGGCCGG	19192
Qy	1159	GGAGGCCATCCCTGGGGGGTGGCGGTGGGGGGGGGCTCGTGGCTTCAACCAACCTCAAGCTC	1218
Db	19193	GGAGGCCATCCCTGGGGGGTGGCGGTGGGGGGGGGCTCGTGGCTTCAACCAACCTCAAGCTC	19252
Qy	1219	CGGAGCTCTCTCGAGGGGCACTGAGAGGCGCGCTCACTCAAGAGGGGCTCAAGCGCTC	1278
Db	19253	CGGAGCTCTCTCGAGGGGCACTGAGAGGCGCGCTCACTCAAGAGGGGCTCAAGCGCTC	19312
Qy	1279	GGCGTCTCGGCTCGCTGGAAGAGCGCATGAGATGGTGTCCAGAGCTTCAACCAAGC	1338
Db	19313	GGCGTCTCGGCTCGCTGGAAGAGCGCATGAGATGGTGTCCAGAGCTTCAACCAAGC	19372
Qy	1339	CTTTCGGCTGTCTCGGGACAAGAAATGGGCAAGTGGCTGCGCGCTCAATCGTAAGATCTT	1398
Db	19373	CTTTCGGCTGTCTCGGGACAAGAAATGGGCAAGTGGCTGCGCGCTCAATCGTAAGATCTT	19432
Qy	1399	TGGGCTCTGCTGGGCCCCATACAAGCTGTAGTATCATCGGGGCGCGCTGCATGGCCA	1458
Db	19433	TGGGCTCTGCTGGGCCCCATACAAGCTGTAGTATCATCGGGGCGCGCTGCATGGCCA	19492
Qy	1459	CTGCGTCCCTGACTACTGTGTAAGAACTTCTCTTGTGGGTCTGTGGGCAACTGGGTGT	1518
Db	19493	CTGCGTCCCTGACTACTGTGTAAGAACTTCTCTTGTGGGTCTGTGGGCAACTGGGTGT	19552
Qy	1519	CAACCCGTCTCTCAACCTCTGTGGCAACAAGCTTTCGCGGGCCCTTACAACAAGCTGT	1578
Db	19553	CAACCCGTCTCTCAACCTCTGTGGCAACAAGCTTTCGCGGGCCCTTACAACAAGCTGT	19612
Qy	1579	CTGCCCCCAGAAAGCTCAAAATTCAGAGCCCAAGCTCCCTGAGACACTGTGGAAGTGA	1638
Db	19613	CTGCCCCCAGAAAGCTCAAAATTCAGAGCCCAAGCTCCCTGAGACACTGTGGAAGTGA	19672
Qy	1639	GGCCCAACAAGGCTCCCTCAGCCAAGCTCTCTCAAGCCCAAGGTCTCTGGGCACTGGC	1698
Db	19673	GGCCCAACAAGGCTCCCTCAGCCAAGCTCTCTCTCAAGCCCAAGGTCTCTGGGCACTGGC	19732
Qy	1699	CTGTGCTGCCCCCTTACCGGCTCTTCCCCAGGGGGTGAAGCCCGCGCTGTGTGGCCCT	1758
Db	19733	CTGTGCTGCCCCCTTACCGGCTCTTCCCCAGGGGGTGAAGCCCGCGCTGTGTGGCCCT	19792
Qy	1759	CTCTTAATGCAAGGAGCAACCCCTGCAATGAGAGGGGCTTCTGTGGTGTGGCAGAGGCG	1818
Db	19793	CTCTTAATGCAAGGAGCAACCCCTGCAATGAGAGGGGCTTCTGTGGTGTGGCAGAGGCG	19852
Qy	1819	CCCTCACTGGCTGACTGAGAGCTGGGTGGCGGACCTGCGCCGCCCAATTTGACTGCAC	1878
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Qy	1879	CGGGAGGAGCACTGTGGAAGTCCCAAGATGTGCCACCCCTGTGTGTGCCACCT	1938
Db	19913	C-GGGAGGAGCACTGTGGAAGTCCCAAGATGTGCCACCCCTGTGTGTGCCACCT	19972
Qy	1939	TGCGAGTTACTGGTGTGGTGTCTTCCCAAGGAAGCACTGGGTGTGCTCCAGGCTTCT	1998
Db	19972	TGCGAGTTACTGGTGTGGTGTCTTCCCAAGGAAGCACTGGGTGTGCTCCAGGCTTCT	20031
Qy	1999	GCCCTAGCAAGTTTGCCTCTGCACGTGCACAACCTGCACAACCCCTGCACAACA	2058
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Qy	2059	CCGTTCCTCTTCCCGGACAAGCCAGGACACTGCTCTTGTGTGCTGTCTTGTGATA	2118
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QY	2119	AGCCTCAGGCGCTGGCCCTTTTCA	CCCCCTTC	CCCA	CAAACTCTCTGTCGCCCAAAAGTGT	2118
Db	20152	AGCCTCAGGCGCTGGCCCTTTTCA	CCCCCTTC	CCCA	CAAACTCTCTGTCGCCCAAAAGTGT	2021
QY	2179	CAAGGGGCGCCTAGGAACCTCGAAGCTGTCTCTGCTTTTCCATCTTGGGTGTTCAGAA				2238
Db	20212	CAAGGGGCGCCTAGGAACCTCGAAGCTGTCTCTGCTTTTCCATCTTGGGTGTTCAGAA				2027
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Db	20272	AGATGAAGAGAAAACATGTCTGTGAA	CTTGATGTTCTGTGGATGTTTAATCAAGAGAGA			2033
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DEFINITION	Sequence 2796 from Patent EP1396543.					
ACCESSION	CQ782656					
VERSION	CQ782656.1	GI:45502599				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE	Homo sapiens					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
	1 Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.					
TITLE	Primer: for synthesizing full length cDNA clones and their use					
JOURNAL	Patent: EP 1396543-A 2796 10-MAR-2004;					
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Query Match 60.6%; Score 1636.2; DB 6; Length 1902;
Best Local Similarity 88.6%; Pred. No. 4.1e-213;
Matches 1899; Conservative 0; Mismatches 3; Indels 241; Gaps 2;

QY 530 ATCTCGACTTCTCGTCGCGCGCTTCTGATCCCACTGATGTAACCTTACGTCGTACA 589
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QY 590 GGCCTGTGACCTTTCGCGCGCGCGCTTCTGAAAGCTTGTGCTGTGATGTAACCTTCTG 649
DB 61 GGCCTGTGACCTTTCGCGCGCGCGCTTCTGAAAGCTTGTGCTGTGATGTAACCTTCTG 120
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RESULT 11
BD127248 1902 bp DNA linear PAT 18-SEP-2002
LOCUS Primer for synthesizing full-length cDNA and use thereof.
DEFINITION
ACCESSION BD127248
VERSION BD127248.1 GI:23222193
KEYWORDS JP 2002017375-A/2679.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1902)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Makamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2679 22-JAN-2002;
HEBIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2679
PD 22-JAN-2002 JP 2000253172
PF 07-JUL-2000 JP 2000253172
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PI YUJI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUO OTSUKI,HISASHI KOGA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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(235) . (864) .
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ORIGIN
Query Match 60.6%; Score 1636.2; DB 6; Length 1902;
Best Local Similarity 88.6%; Pred. No. 4,1e-213;
Matches 1899; Conservative 0; Mismatches 3; Indels 241; Gaps 2;

QY 530 ATCTCGACCTCTCTGTCGGGCGCTTCTGCATCCACTGTATGACCTTACGTCGACA 589
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RESULT 12
AK074730
LOCUS AK074730 1902 bp mRNA linear PRI 03-SEP-2002
DEFINITION Homo sapiens cDNA FLJ90249 f1s, clone NT2RM2001941, weakly similar
to MUSCRINIC ACETYLCHOLINE RECEPTOR M1.
ACCESSION AK074730
VERSION AK074730.1 GI:22760362
KEYWORDS oligo capping, f1s (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsubu,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahara,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotsuma,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1902)
AUTHORS Isogai,T. and Otsubu,T.

TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction;
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection; Helix Research Institute (supported
by Japan Key Technology Center etc.).
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Query Match 60.6%; Score 1636.2; DB 9; Length 1902;
Best Local Similarity 88.6%; Pred. No. 4.1e-213;
Matches 1899; Conservative 0; Mismatches 3; Indels 241; Gaps 2;
QY 530 ATCTCCGACTTCTGCTGCGGCGCTTCTGACATCCACATGATATGATACCTACGCTGAC 589
DB 1 ATCTCCGACTTCTGCTGCGGCGCTTCTGACATCCACATGATATGATACCTACGCTGAC 60
QY 590 GGGCGGTGACCTTGGGCGGCGCTTCTGACAGCTGTGCTGTGATGATGATACCTGCTG 649
DB 61 GGGCGGTGACCTTGGGCGGCGCTTCTGACAGCTGTGCTGTGATGATGATACCTGCTG 120
QY 650 TGCACCTCTCTGCTGCTTCAACATGAGCTCATGAGTACAGACCGCTTCTGCTGCTGACC 709
DB 121 TGCACCTCTCTGCTGCTTCAACATGAGCTCATGAGTACAGACCGCTTCTGCTGCTGACC 180
QY 710 CGAGCGGTCTCAATCCGCGCCAGAGAGGTGACACGCGCGGCGAGTGCAGAGATGCTG 769
DB 181 CGAGCGGTCTCAATCCGCGCCAGAGAGGTGACACGCGCGGCGAGTGCAGAGATGCTG 240
QY 770 CTGCTGTGGGTCTGGGCTTCTGCTGTACGACACGACCATCTGAGCTGGAGATGACTG 829
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QY 830 TCCGGGGGAGCTCCATCCCGAGGGGCACTGCTATGCGGAGTTCTTCAACACTGGTAC 889
DB 301 TCCGGGGGAGCTCCATCCCGAGGGGCACTGCTATGCGGAGTTCTTCAACACTGGTAC 360
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DB 361 TTCTTCATCAGCGCTTCCACCTGAGATTTCTTACGCTTCTGACGCTCACTTCTTT 420
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DB 421 AACCTCAGATTTACTGAATCAACAGAGGCGACCCGCTTCCGCTGGATGGGCTGCA 480
QY 1010 GAGGAGCGCGCGCGCGCGCGCTTCCGAGGGCGAGGCTTACACCCCAACCGCTGCG 1069
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QY	1070	TGCTGGGGCTGTGGCAGAAAGGGGACCGGGAGGCCATGCGCTGACAGAGATGGGGTG	1127
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DB	661	ATGATCATCCGGGCGGCGCTGACATGAGCCATCTGCTCCCTGACTATGTTGTAAGAACTCC	720
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DB	781	AGCTTCGCGCGGCGCTTGCACCAAGCTGTGCTGCCCCGAGAGCTCAAAATCAGCCCCAC	840
QY	1610	AGCTCCCTGAGAGCATGTCTGGAAGTGAATGAGGCCACAGAGCTCTCCCTACGACGCTC	1668
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DB	901	TCTAAGCCCAAGTCTCTGGGCACTGTGGCCCGCTGTGGCCCGCTACCCGGCTGTTCCGCCA	960
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QY	1790	GAGGCGCTTCTGTGGTGGCCAGAGGGCCCTCTCTAGTGAAGCTGAGGCTGTGGTGGC	1849
DB	1021	GAGGCGCTTCTGTGGTGGCCAGAGGGCCCTCTCTAGTGAAGCTGAGGCTGTGGTGGC	1080
QY	1850	CGGCGCTGGCCCCCACTTGTGGCTTCAACGGGAGGAGCATGTGGAAGTCCAGAT	1909
DB	1081	CGGCGCTGGCCCCCACTTGTGGCTTCAAC--GGAGGAGCATGTGGAAGTCCAGAT	1139
QY	1910	GCTGCGCACCCCTGTGCTGTGGCCACCTTGCAGATTAATGTGGTGGTTCCTTCCCAAG	1969
DB	1140	GCTGCGCACCCCTGTGCTGTGGCCACCTTGCAGATTAATGTGGTGGTTCCTTCCCAAG	1139
QY	1970	CAAGCACTGGAGTGTCTCAGAGCTTCTGCGCTTAGCAGTTCCTGTGACGTGACAC	2029
DB	1200	CAAGCACTGGAGTGTGTCTCAGAGGCTTCTGCGCTTAGCAGTTCCTGTGACGTGACAC	1259
QY	2030	ACCTGCAACCCCTGTGACACACCTGACACACGTCCCTTCCCCGGACAGGCCAGAGAC	2089
DB	1260	ACCTGCAACCCCTGTGACACACCTGACACACGTCCCTTCCCCGGACAGGCCAGAGAC	1319
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Query Match 58.9%; Score 1590.2; DB 6; Length 1893;
Best Local Similarity 98.5%; Pred. No. 7.4e-207;
Matches 1615; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

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DEFINITION Sequence 13 from patent US 6750322.
ACCESSION ARS59681
VERSION ARS59681.1 GI:53969737
KEYWORDS
SOURCE
ORGANISM Unknown.
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1 (bases 1 to 1893)
AUTHORS Itadani,H., Takimura,T., Nakamura,T., Kobayashi,M., Tanaka,K.-I.,
Hidaka,Y. and Ohwa,M.
TITLE Guanosine triphosphate (GTP) binding protein-coupled receptor
proteins
JOURNAL Patent: US 6750322-A 13 15-JUN-2004;
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Query Match 58.9%; Score 1590.2; DB 6; Length 1893;
Best Local Similarity 98.5%; Pred. No. 7.4e-207;
Matches 1615; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

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316 TACAACGCGCGGGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 375
799 CGGACGAGCCTCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 858
376 CGGACGAGCCTCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 435
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Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Cercopithecinae; Macaca.
1 (bases 1 to 1600)
Yao, B.B., Sharma, R., Casar, S., Espenshade, T.A., Hancock, A.A.,
Cloning and Pharmacological Characterization of the Monkey
Histamine H3 Receptor
Unpublished
2 (bases 1 to 1600)
Casar, S., Espenshade, T.A., Hancock, A.A., and Yao, B.B.
Direct Submision
JOURNAL
Submitted (07-FEB-2003) R-4MN, Abbott Laboratories, AP9A, 100
Abdott Park Road, Abdott Park, IL 60064, USA
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Query Match      55.1%; Score 1486.6; DB 9; Length 1600;
Best Local Similarity 95.9%; Pred. No. 9.4e-193;
Matches 1536; Conservative 0; Mismatches 64; Indels 1; Gaps 1;

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QY 1737 GCCCGCGCGTGTCTGTGCGCGCTCTCTTAAATGCGAGCGGAGC 1777
DB 1560 GCCCGCGCGTGTGTGTGCGCGCTCTCTTAAATGCGAGCGGAGC 1600

```

Search completed: June 2, 2005, 10:53:01
 Job time : 11703.2 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 04:43:59 ; Search time 1440.49 Seconds
(without alignments)
11091.610 Million cell updates/sec

Title: US-10-727-021-5

Perfect score: 2699
Sequence: 1 ccacgcgcgcgcgcgtcga.....aaaaaaaaaaaaaaaaaaaaa 2699

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2699	100.0	2699	3	AAA09061 Human his
2	2699	100.0	2699	4	AAC62365 Complete
3	2699	100.0	2699	6	ABN84882 Human his
4	2699	100.0	2699	8	ABZ42533 Human his
5	2699	100.0	2699	9	ACC59394 Human his
6	2699	100.0	2699	10	ACC59394 Human his
7	2699	100.0	2699	13	ADD22860 Human ful
8	2699	100.0	2699	13	ADQ89179 Human his
9	2699	100.0	2699	13	ADR31456 Human his
10	2699	100.0	2699	13	ADR31456 Human his
11	2699	100.0	2699	13	ADR31456 Human his
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13	2699	100.0	2699	13	ADR31456 Human his
14	2699	100.0	2699	13	ADR31456 Human his
15	2699	100.0	2699	13	ADR31456 Human his
16	2699	100.0	2699	13	ADR31456 Human his
17	2699	100.0	2699	13	ADR31456 Human his
18	2699	100.0	2699	13	ADR31456 Human his
19	2699	100.0	2699	13	ADR31456 Human his
20	2699	100.0	2699	13	ADR31456 Human his

21	1384.8	51.3	3244	2	AAH44574	AAH44574 Rat musca
22	1384.8	51.3	3244	8	ABX11853	ABX11853 Rat cdna
23	1360.4	50.4	2050	3	AAH84572	AAH84572 Human G-P
24	1360.4	50.4	2050	3	AAH70637	AAH70637 Human G-P
25	1358.8	50.3	2761	10	ABT42301	ABT42301 Toxicity
26	1348.4	50.0	2483	12	ADO30256	ADO30256 Mouse GPC
27	1336.4	49.5	1338	12	ADO29966	ADO29966 Human GPC
28	1335	49.5	1335	3	AAH09062	AAH09062 Human his
29	1335	49.5	1335	4	AAC62366	AAC62366 CDNA enco
30	1335	49.5	1335	5	ACC59395	ACC59395 Human his
31	1335	49.5	1335	10	ADD22861	ADD22861 Human his
32	1335	49.5	1335	13	ADR31457	ADR31457 Human his
33	1331.8	49.3	1335	2	AAH02886	AAH02886 Human his
34	1330.8	48.3	1334	2	AAH44573	AAH44573 Human his
35	1303.8	48.3	1359	9	AAH59978	AAH59978 Human his
36	1272.6	47.2	1293	9	AAH59982	AAH59982 Human his
37	1208	44.8	2700	3	AAH70640	AAH70640 Rat G-pro
38	1207.8	44.7	1311	9	AAH59979	AAH59979 Human his
39	1204.8	44.6	2700	2	AAH84571	AAH84571 G-protein
40	1201.8	44.5	1953	3	AAH70638	AAH70638 Rat G-pro
41	1178.6	43.7	1251	9	AAH59983	AAH59983 Human his
42	1156	42.8	2145	5	AAH76868	AAH76868 DNA enco
43	1082.6	40.1	1203	5	AAH59985	AAH59985 Human his
44	1075.2	39.8	1805	8	ABZ82337	ABZ82337 Mouse his
45	1072.2	39.7	1338	2	AAH44575	AAH44575 Rat musca

ALIGNMENTS

RESULT 1	AAA09061	standard; cdna; 2699 BP.
ID	AAA09061	standard; cdna; 2699 BP.
AC	AAA09061	
DT	10-AUG-2000	(first entry)
XX	Human histamine H3 receptor cdna.	
XX	histamine H3 receptor; biogenic amine receptor homologue; ss.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	CDS	299..1636
XX	FT	/*tag= a
XX	FT	/product= "histamine_H3_receptor"
XX	PN	WO200020011-A1.
XX	PD	13-APR-2000.
XX	PF	07-OCT-1998; 98WO-US021090.
XX	PR	07-OCT-1998; 98WO-US021090.
XX	PA	(ORTH) ORTHO-MCNELL PHARM INC.
XX	PI	Lovenberg TW, Erlander M, Huvar A, Pyati J;
XX	DR	WPI; 2000-303632/26.
XX	DR	P-PSDB; AAY92218.
XX	PT	Novel human histamine H3 receptor polynucleotides and polypeptides used
XX	PT	in methods to identify modulators of receptor activity.
XX	PS	Claim 2; Fig 1A-B; 54pp; English.
XX	CC	The CDNA encodes the human histamine H3 receptor. The polypeptide
XX	CC	contains the seven conserved hydrophobic domains and specific residues
XX	CC	conserved in biogenic amine receptors. The human histamine H3 receptor
XX	CC	polynucleotides and polypeptides are used in methods to screen for

modulators of receptor activity (claimed). Such agonists and antagonists may prove useful as research tools or may be used as therapeutics to treat disorders directly or indirectly involving histamine receptors (claimed). The characterization of the polymorphic histamine receptors (claimed) for forensic analysis, diagnostic applications, and epidemiological studies

Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;

Query Match 100.0%; Score 2699; DB 3; Length 2699;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCAACGCTCCGCGGCTGACAGGTCACCCGAGCGGCTCAGGCTCCGCTCTCTCC 60
DB 1 CCAACGCTCCGCGGCTGACAGGTCACCCGAGCGGCTCAGGCTCTCTCTCC 60
QY 61 GCTGACAGCCGCGCTGCGGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 120
DB 61 GCTGACAGCCGCGCTGCGGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 120
QY 121 CCGGCTGCTTGGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGG 180
DB 121 CCGGCTGCTTGGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGG 180
QY 181 ACCCGACCCGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGGCG 240
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DB 301 GGAAGCGCGCGCGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGGCGG 360
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DB 361 GAGCGCGCGCGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGGCGGCG 420
QY 421 GCGGCTGCTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 480
DB 421 GCGGCTGCTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 480
QY 481 CCACTGAGGCTCCGACCCAGAACAACTTCTTCTGCTCAACTGCGGCTCCG 540
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QY 541 CCTGCTGCGGCTTCTGTCATCCACTGTATGTAACCTTACGTCGACAGCG 600
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DB 1021 CCGCGAGCCCGCTCCGAGGCGGCGGCGGCTCCGCGTCGTATGCGGCTCCAGAG 1080
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QY 1141 CCGAGGCGGTCGAGGCGGCGGCGGCGGCGGCTCCGCGTCGTATGCGGCTCCAGAG 1200
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QY 1201 TTCAACCACTTCAGCTCCGCGGCTCCGAGGCGGCGGCTCCGCGTCGTATGCGGCTCCAGAG 1260
DB 1201 TTCAACCACTTCAGCTCCGCGGCTCCGAGGCGGCGGCTCCGCGTCGTATGCGGCTCCAGAG 1260
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DB 1261 GAGGCGGCTCCAGGCGGCGGCGGCGGCGGCTCCGCGTCGTATGCGGCTCCAGAG 1320
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QY 1381 CCGTATGTCGAGCATTTTGGGCTCTGTCGCGGCGGCGGCTCCGCGTCGTATGCGGCTCCAGAG 1440
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DB 1441 GCGCGCTGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1500
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QY 1921 CTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1980
DB 1921 CTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1980
QY 1981 GTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2040
```


KW antiallergic; antiinflammatory; gene therapy; gene; ss.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 299..1636
FT /*tag= a
FT /product= "Histamine H3 receptor"
XX
XX US6413743-B1.
XX
XX 02-JUL-2002.
XX
XX 21-AUG-2000; 2000US-00642855.
XX
XX 07-OCT-1998; 98US-00167354.
XX
XX (ORTH) ORTHO PHARM CORP.
XX
XX Lovenberg TW, Erlander M, Huvar A, Pyati J;
XX WPI; 2002-641560/69.
XX P-PSDB; ABB79792.
XX
XX Novel isolated and purified DNA molecule encoding human histamine H3
PT receptor protein, useful for identifying modulators of human histamine H3
PT receptor protein activity.
XX
XX Example 3; Fig 1A-B; 25pp; English.
XX
XX The present sequence is that of cDNA clone pH3 coding for human
CC histamine H3 receptor, a novel G-protein coupled receptor. The clone was
CC isolated from a human thalamus cDNA library using a histamine H3 receptor
CC probe. Histamine H3 receptor cDNA has been expressed in recombinant host
CC cells, which produced active recombinant protein. H3 receptor nucleic
CC acids and proteins can be used to identify modulators of H3 receptor
CC activity or expression, useful as therapeutic or diagnostic agents for
CC central nervous system disorders, such as depression, anxiety, psychoses
CC (e.g. schizophrenia), cardiac dyskinesia, Parkinson's disease, obesity,
CC hypertension, Tourette's syndrome, sexual dysfunction, drug addiction,
CC drug abuse, cognitive disorders, Alzheimer's disease, senile dementia,
CC obsessive-compulsive behaviour, panic attacks, pain, social phobias,
CC eating disorders and anorexia, cardiovascular and cerebrovascular
CC disorders, non-insulin dependent diabetes mellitus, hyperglycaemia,
CC constipation, arrhythmia, disorders of the neuroendocrine system, stress
CC and spasticity, as well as acid secretion, ulcers, airway constriction,
CC asthma, allergy, inflammation and prostate dysfunction. Histamine H3
CC receptor DNA molecules are also useful for isolating related sequences,
CC identifying and isolating genomic equivalents, identifying, detecting or
CC isolating mutant forms of DNA, and in gene therapy
XX
XX Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 2699; DB 6; Length 2699;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACGCGTCGCGCGCTGCAAGTCCGACCGGAGCGGCTCAAGCTCCGCTCTCTCC 60
Db 1 CCAAGGTGTCGCGCGCTGCAAGTCCGACCGGAGCGGCTCAAGCTCTCTCTCC 60
QY 61 GCTGCAAGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db 61 GCTGCAAGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 121 CGGCGCTGCTGCG 180
Db 121 CGGCGCTGCTGCG 180
QY 181 ACCGAGCCCG 240
Db 181 ACCGAGCCCG 240

QY 241 CCAGCTCTGCG 300
Db 241 CCAGCTCTGCG 300
QY 301 GGAAGCG 360
Db 301 GGAAGCG 360
QY 361 GCG 420
Db 361 GCG 420
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Db 601 CTTGCG 660
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QY 721 ATACCG 780
Db 721 ATACCG 780
QY 781 GCGCGCGCTTCTGTCGTCATGTCGTCATGTCGTCATGTCGTCATGTCGTCAT 840
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QY 841 CTCATCCCCGAGGCG 900
Db 841 CTCATCCCCGAGGCG 900
QY 901 GCGCTTCAACATGTCGTCATGTCGTCATGTCGTCATGTCGTCATGTCGTCAT 960
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QY 1081 CTGCGAAGAGGCG 1140
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QY 1141 CGTAGCGCTGAGGCG 1200
Db 1141 CGTAGCGCTGAGGCG 1200
QY 1201 TTCAACCACTCTCAAGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
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QY 1261 GAGGCGCTTCAAGCG 1320
Db 1261 GAGGCGCTTCAAGCG 1320
QY 1321 CCAAGCTTCAACCG 1380

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Db      1381  CGTCAATCGAGCATTTTGGGCTGTGGGCCCCATACAGCTGTATGATCATCCG 1440
Qy      1441  GGCCGCTCCCAATGCGCACTGCGTCCCTGACTACTGTGTAAGAACTCTTCTGTGCT 1500
Db      1441  GGCCGCTCCCAATGCGCACTGCGTCCCTGACTACTGTGTAAGAACTCTTCTGTGCT 1500
Qy      1501  GTGGGCAATGCGGCTGTAACCTGTCTCTAACCCTGTGTGCAACAGCTCCGCG 1560
Db      1501  GTGGGCAATGCGGCTGTAACCTGTCTCTAACCCTGTGTGCAACAGCTCCGCG 1560
Qy      1561  GGCCTTACCAAGCTCTGCCCCCAAGAGCTCAAAATCCAGCCCCCAAGCTCCCTGA 1620
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Qy      1621  GCACTGTGGAAGTGAAGTGGCCCAAGAGCCCTCCCTGAGCCAGGCTCTTCAAGCCAG 1680
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Qy      1681  GTCTCTGGGCAATGCGGCTGTGCCCCCTACCCGCTGTCCCTCCGAGGGGTGAGCC 1740
Db      1681  GTCTCTGGGCAATGCGGCTGTGCCCCCTACCCGCTGTCCCTCCGAGGGGTGAGCC 1740
Qy      1741  GCGCGTGTGAGGCTCTCTTAAATGCCAGGACAGCCCTCCCTGAGCCAGGCTCTTCA 1800
Db      1741  GCGCGTGTGAGGCTCTCTTAAATGCCAGGACAGCCCTCCCTGAGCCAGGCTCTTCA 1800
Qy      1801  CTGGGTTGGCCAGAGGCCCCCTCACTGAGTGAATGGAAGCTGTGGGCTCCGCTCC 1860
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Qy      1861  CCGCATTTCTGCTCTCAACCGGGAGAGAGATGTGAAAGTCCCAACATGCTGCCACCC 1920
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Db      1921  CCGTGTGAGGCTCCCTTCGACGATTAAGTGTGTTGTTTCCCAAAGCAAGCACTGG 1980
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Db      2041  CCGTGCACACCTGCACACCGTCCCTTCCCGGACAAAGCCAGAGCACTGCTTTGCTG 2100
Qy      2101  CCGTGTGCTGTGACATTAAGCTCAGGCTGAGCCCTTTCACCCCTTCCCAACCACTT 2160
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Qy      2161  CTTCTGTCTCTTGTGACATTAAGCTCAGGCTGAGCCCTTTCACCCCTTCCCAACCACTT 2220
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Qy      2221  TTTCTGGGTTTTCAGAAAGATGAAGAAACAAAGTGTGAAATTTATGTATGTCTGGG 2280
Db      2221  TTTCTGGGTTTTCAGAAAGATGAAGAAACAAAGTGTGAAATTTATGTATGTCTGGG 2280
Qy      2281  ATGTTTAATCAAGAGAGCAAAATGCTGAGAGCTCAGGCTGATGTGGAGGTGGG 2340
Db      2281  ATGTTTAATCAAGAGAGCAAAATGCTGAGAGCTCAGGCTGATGTGGAGGTGGG 2340
Qy      2341  CTCCACGCGCTCTTCCCTCCGCTAAGAGCTTCGCGGTGAAGCTGTGCAAGCTCTTCTG 2400
Db      2341  CTCCACGCGCTCTTCCCTCCGCTAAGAGCTTCGCGGTGAAGCTGTGCAAGCTCTTCTG 2400
Qy      2401  CACCCGCTCTGGGCTCACACGAGCTGTGTGCTCAAGCTGCCCCGACCTCTGTTT 2460

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Db      2401  CACCCGCTCTGGGCTACACACGACCTGTGTGCCAAAGCTGCCCGGCACTGTGTT 2460
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Db      2461  GCTCACCCAGAGACCTCTGAGGAGTTGTGGAAGAGGAGGCGCGCTGGGCTCCAGGATCC 2520
Qy      2521  CAAGGCTGACAGGAGGCGGTCCAGAGAGTCCCGGAGAGGAGGCGCTTCCGCAATGTGT 2580
Db      2521  CAAGGCTGACAGGAGGCGGTCCAGAGAGTCCCGGAGAGGAGGCGCTTCCGCAATGTGT 2580
Qy      2581  GTGACCCGCTGACAGGCGCTGACAGTCCCTCTGCTGTGCGCGCTGCGCTGCA 2640
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Qy      2641  AACCGTAGTGCACATTAAGTATTTTAAAAA 2699
Db      2641  AACCGTAGTGCACATTAAGTATTTTAAAAA 2699

RESULT 4
AB242533
ID   AB242533 standard; DNA; 2699 BP.
XX
XX   AB242533;
AC
XX   04-MAR-2003 (first entry)
DT
XX
XX   Human histamine H3 receptor nucleotide SEQ ID NO:548.
DE
XX
XX   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor; modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW   ulcer; gene; ds.
XX
XX   Homo sapiens.
OS
XX   WO200261087-A2.
PN
XX
XX   08-AUG-2002.
PD
XX
XX   19-DEC-2001; 2001MO-US050107.
PF
XX
XX   19-DEC-2000; 2000US-0257144P.
PR
XX
XX   (LIFE-) LIFESPAN BIOSCIENCES INC.
PA
XX
XX   Burner GC, Roush CL, Brown JP;
PI
XX
XX   WPI; 2003-046718/04.
DR
XX
XX   P-PSDB; ABP81687.
DR
XX
XX   New isolated antigenic peptides e.g., for G protein-coupled receptors
PT   (GPCR), useful for diagnosing and designing drugs for treating conditions
PT   in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT   autoimmune diseases.
PS
XX
XX   Disclosure; Fig 1; 523pp; English.
XX
XX   The present invention describes antigenic peptides (I) comprising: (a)
CC   any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC   acids. Also described: (1) an assay for the detection of a particular G
CC   protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC   and (2) an isolated antibody having high specificity and high affinity or
CC   avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC   gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC   antibody against a particular GPCR, and in the production of specific

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antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacteriosis, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. AB242523 to AB24859 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention

Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;

Query Match 100.0%; Score 2699; DB 8; Length 2699;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCACGCGTCCGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 60
1 CCAAGGCTCCGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 60
61 GCTGAGACGCGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 120
61 GCTGAGACGCGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 120
121 CCGGCTGCTGCGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 180
121 CCGGCTGCTGCGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 180
181 ACCGACCGGCGGACGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 240
181 ACCGACCGGCGGACGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 240
241 CCGGCTGCTGCGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 300
241 CCGGCTGCTGCGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 300
301 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 360
301 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 360
361 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 420
361 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 420
421 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 480
421 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 480
481 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 540
481 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 540
541 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 600
541 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 600
601 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 660
601 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 660
661 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 720
661 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 720
721 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 780

721 ATACCGGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 780
781 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 840
781 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 840
841 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 900
841 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 900
901 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 960
901 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 960
961 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1020
961 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1020
1021 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1080
1021 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1080
1081 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1140
1081 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1140
1141 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1200
1141 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1200
1201 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1260
1201 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1260
1261 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1320
1261 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1320
1321 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1380
1321 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1380
1381 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1440
1381 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1440
1441 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1500
1441 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1500
1501 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1560
1501 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1560
1561 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1620
1561 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1620
1621 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1680
1621 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1680
1681 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1740
1681 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1740
1741 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1800
1741 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1800
1801 GGAAGCGCGGCGGCTGCAAGTCCGACCGGACGCGCTCAGGCTCCGCTCTCC 1860

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Db 1801 CTGGGTTGGCCAGAGGAGCCCTCACTGCTGGACTGAGAGCTGGAGGCCGCGCTGCC 1860
Oy 1861 CCCACATTCGTGCTCCACCGGAGGAGGAGAGTCTGAGAGTCCACAGCATGCTGCCACCC 1920
Db 1861 CCCACATTCGTGCTCCACCGGAGGAGGAGAGTCTGAGAGTCCACAGCATGCTGCCACCC 1920
Oy 1921 CCTGCTGCTGCTCCACCGGAGGAGGAGTCTGAGAGTCTGAGAGTCCACAGCATGCTGCC 1980
Db 1921 CCTGCTGCTGCTCCACCGGAGGAGGAGTCTGAGAGTCTGAGAGTCCACAGCATGCTGCC 1980
Oy 1981 GTGTGCTGAGGCTTCCTGCTGAGAGTCTGAGAGTCTGAGAGTCCACAGCATGCTGCC 2040
Db 1981 GTGTGCTGAGGCTTCCTGCTGAGAGTCTGAGAGTCTGAGAGTCCACAGCATGCTGCC 2040
Oy 2041 CCTGACACACCTGACACAGCTGCTCCCTCCGAGCAAGCCACAGACATGCTGCTGCTG 2100
Db 2041 CCTGACACACCTGACACAGCTGCTCCCTCCGAGCAAGCCACAGACATGCTGCTGCTG 2100
Oy 2101 CCTTCTGCTCTTTCGATTAAGCTCAGGCTGAGGCTGCTTCACTTCCACCACTCT 2160
Db 2101 CCTTCTGCTCTTTCGATTAAGCTCAGGCTGAGGCTGCTTCACTTCCACCACTCT 2160
Oy 2161 CTCTGCTGCTCTTTCGATTAAGCTCAGGCTGAGGCTGCTTCACTTCCACCACTCT 2220
Db 2161 CTCTGCTGCTCTTTCGATTAAGCTCAGGCTGAGGCTGCTTCACTTCCACCACTCT 2220
Oy 2221 TTCTGCTGCTCTTTCGATTAAGCTCAGGCTGAGGCTGCTTCACTTCCACCACTCT 2280
Db 2221 TTCTGCTGCTCTTTCGATTAAGCTCAGGCTGAGGCTGCTTCACTTCCACCACTCT 2280
Oy 2281 ATGTTTATCAAGAGAGACAAATTCCTGAGAGCTCAGGCTGAGGCTGAGGCTGAGG 2340
Db 2281 ATGTTTATCAAGAGAGACAAATTCCTGAGAGCTCAGGCTGAGGCTGAGGCTGAGG 2340
Oy 2341 CTCCCAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2400
Db 2341 CTCCCAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2400
Oy 2401 CACCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
Db 2401 CACCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
Oy 2461 GCTCAACCCAGAGCTCTGAGGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2520
Db 2461 GCTCAACCCAGAGCTCTGAGGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2520
Oy 2521 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
Db 2521 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
Oy 2581 GTGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Db 2581 GTGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Oy 2641 AACCGTAGCTCAATTAAGTATTTTAAAAA 2699
Db 2641 AACCGTAGCTCAATTAAGTATTTTAAAAA 2699

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RESULT 5
 ACC59394
 ID ACC59394 standard; DNA; 2699 BP.
 XX AC ACC59394;
 XX 28-AUG-2003 (first entry)
 XX Human histamine H3 receptor nucleotide sequence.
 XX
 XX Human histamine H3 receptor; gene; ds; agonist;
 KW neurotropic; neuroprotective; cerebroprotective; cardiant; antidiabetic;
 KW immunomodulator; gastrointestinal; antiallergic; antidiabetic;
 KW antiinflammatory; hypotensive; antiarrhythmic.

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XX OS Homo sapiens.
XX PN MO2003044059-A1.
XX PD 30-MAY-2003.
XX PF 15-NOV-2001; 2001WO-US045313.
XX PR 15-NOV-2001; 2001WO-US045313.
XX PA (ORTH ) ORTHO-MCNEIL PHARM INC.
XX PI Lovenberg T;
XX DR MPI; 2003-457595/43.
XX PT Identifying agonists of recombinant human histamine H3 receptor protein
XX PT activity, useful for diagnosing and treating H3 receptor-related
XX PT disorders, such as nervous system disorders, asthma, allergy,
XX PT hypertension and diabetes.
XX PS Example 1; Fig 1; 55pp; English.
XX CC The present invention relates to a method of identifying compounds that
XX CC are agonists of recombinant human histamine H3 receptor protein activity,
XX CC comprising combining a compound suspected of being an antagonist of human
XX CC histamine H3 receptor protein activity with recombinant human histamine
XX CC H3 receptor protein, and measuring an agonistic effect of the compound on
XX CC the recombinant human histamine H3 receptor protein. The methods and
XX CC compositions of the present invention are useful for diagnosing and
XX CC treating human histamine H3 receptor-related disorders, such as central
XX CC and peripheral nervous system disorders (depression, anxiety, psychosis,
XX CC Parkinson's disease, Alzheimer's disease, dementia and tardive
XX CC dyskinesia), asthma, allergy, diabetes mellitus, inflammation, immune,
XX CC cardiovascular (hypertension, and arrhythmia) and gastrointestinal
XX CC disorders. The present sequence is the coding sequence of the human
XX CC histamine H3 receptor
XX SQ Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;

Query Match 100.0%; Score 2699; DB 9; Length 2699;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCACGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 1 CCACGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Oy 61 GCTGACAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 GCTGACAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Oy 121 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 121 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Oy 181 ACCCGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 ACCCGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Oy 241 CCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 241 CCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Oy 301 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 301 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Oy 361 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

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[illegible]

Db	1501	GTGGAGCAACTGGACTGTCAACCTGTGCTCTTACCTCTGTGGACAACAAGCTTCGGCG	1560
Oy	1561	GGCCCTTCAACAAGCTGTGCTGCCCCAGAAAGCTCAAAATCAGAGCCCAAGCTCCCTGA	1620
Db	1561	GGCCTTCAACAAGCTGTGCTGTCCCCAGAAAGCTCAAAATCAGAGCCCAAGCTCCCTGA	1620
Oy	1621	GCACGTGTGAAAGTAGAGTGAGGCCACAGAGGCTCCTCAGGCAAGCTCTCTCAGCCAG	1680
Db	1621	GCACGTGTGAAAGTAGAGTGAGGCCACAGAGGCTCCTCAGGCAAGCTCTCTCAGCCAG	1680
Oy	1681	GTCCTCTGGAGATCTTGAGCCCTGTGCCCCCTTACCCGCTGTTCCCAAGGAGTGAACCC	1740
Db	1681	GTCCTCTGGAGATCTTGAGCCCTGTGCCCCCTTACCCGCTGTTCCCAAGGAGTGAACCC	1740
Oy	1741	CGCCGTGTCTGTGAGCCCTCTCTTAATATGCAACGAGGCAACCTTGCATATGAGAGGCGCTTC	1800
Db	1741	CGCCGTGTCTGTGAGCCCTCTCTTAATATGCAACGAGGCAACCTTGCATATGAGAGGCGCTTC	1800
Oy	1801	CTGGGATTGACCAAGAGGAGCCCTCACTGAGCTGAGCTGAGAGGCTGAGGAGCCCTGACC	1860
Db	1801	CTGGGATTGACCAAGAGGAGCCCTCACTGAGCTGAGCTGAGAGGCTGAGGAGCCCTGACC	1860
Oy	1861	CCCAATTTCTGAGCTTCAACCGAGGAGGAGCAAGCTGTGAGAGTCCCAAGAAATGTGCCCCACC	1920
Db	1861	CCCAATTTCTGAGCTTCAACCGAGGAGGAGCAAGCTGTGAGAGTCCCAAGAAATGTGCCCCACC	1920
Oy	1921	CCTGCTGAGTGGCCAAACCCCTTGAGCAATTACGTGTTGATGTTCTTCCCAAGCAAGCACTGG	1980
Db	1921	CCTGCTGAGTGGCCAAACCCCTTGAGCAATTACGTGTTGATGTTCTTCCCAAGCAAGCACTGG	1980
Oy	1981	GTCGTGCTCAGAGCTTCTGTGCCCTAGACAGTTTGCTCTGTGACAGTGACACAACCTGACACCC	2040
Db	1981	GTCGTGCTCAGAGCTTCTGTGCCCTAGACAGTTTGCTCTGTGACAGTGACACAACCTGACACCC	2040
Oy	2041	CTTGACACAACCTGACACAACCGTCTCTCCCCGAGCAAGCCACAGAACACATGCTCTTGTGCTG	2100
Db	2041	CTTGACACAACCTGACACAACCGTCTCTCCCCGAGCAAGCCACAGAACACATGCTCTTGTGCTG	2100
Oy	2101	CCCTCTGTGCTCTTGCAATTAAGCTTCAAGGAGCTGAGGCCCTTTCACCCCTCTTCCACCAACTCT	2160
Db	2101	CCCTCTGTGCTCTTGCAATTAAGCTTCAAGGAGCTGAGGCCCTTTCACCCCTCTTCCACCAACTCT	2160
Oy	2161	CTGTGAGCCCAAAAGTGTCAAGAGGAGCCCTAGAAAGCTTCGAAGCTGTTCTGTGCTTTTCCA	2220
Db	2161	CTGTGAGCCCAAAAGTGTCAAGAGGAGCCCTAGAAAGCTTCGAAGCTGTTCTGTGCTTTTCCA	2220
Oy	2221	TTCTGGAGTGTTTTCAGAAAGATGAAGAAAGAAACATGTCTGTGAACTTGATGTTGCTGAGG	2280
Db	2221	TTCTGGAGTGTTTTCAGAAAGATGAAGAAAGAAACATGTCTGTGAACTTGATGTTGCTGAGG	2280
Oy	2281	ATGTTTAAATCAAGAGAACAAAAATTTGCTGAGAGACTCAAGGGCTGGAATTTGGCAGGTGTGAGG	2340
Db	2281	ATGTTTAAATCAAGAGAACAAAAATTTGCTGAGAGACTCAAGGGCTGGAATTTGGCAGGTGTGAGG	2340
Oy	2341	CTGCCAAGGCCCTCTCCCTCCGCTTAAAGGCTTCCGAGCTGAGCTGTGAGCTGAGCTCTTGTGCC	2400
Db	2341	CTGCCAAGGCCCTCTCCCTCCGCTTAAAGGCTTCCGAGCTGAGCTGTGAGCTGAGCTCTTGTGCC	2400
Oy	2401	CACCCGAGCTCTTGAGGCTCAACAACGAGCCCTGATGAGCCAAAGCTGAGCCGAGCACTCTGTTT	2460
Db	2401	CACCCGAGCTCTTGAGGCTCAACAACGAGCCCTGATGAGCCAAAGCTGAGCCGAGCACTCTGTTT	2460
Oy	2461	GCTTACCCAGAGACCTCTGAGGAGTGTGTTGGAGAGAGGAGGAGCCCGAGCTGAGGAGGAGTCC	2520
Db	2461	GCTTACCCAGAGACCTCTGAGGAGTGTGTTGGAGAGAGGAGGAGCCCGAGCTGAGGAGGAGTCC	2520
Oy	2521	CAAGGAGCTGACAGGAGGAGGAGCTCAAGAGAGTGTCCCGAGCAAGGAGCCGCTTGTGCATATGTGCT	2580
Db	2521	CAAGGAGCTGACAGGAGGAGGAGCTCAAGAGAGTGTCCCGAGCAAGGAGCCGCTTGTGCATATGTGCT	2580
Oy	2581	GTCGACCTGTGACACGAGGCTCTGATGCTCTCTGCTGTGAGCCGAGCTGAGCTGTGCTCTGCA	2640
Db	2581	GTCGACCTGTGACACGAGGCTCTGATGCTCTCTGCTGTGAGCCGAGCTGAGCTGTGCTCTGCA	2640

DB 2581 GTGACACCCGTGCGACGCGCTGTGCATGCTCTGCTGTGCTGCCGCTGCGCTGCGCTGCA 2640
QY 2641 AACCGTGAAGTCAATTAAGTATTTTAAAAA 2699
DB 2641 AACCGTGAAGTCAATTAAGTATTTTAAAAA 2699
RESULT 6
ADD22860
ID ADD22860 standard; cDNA; 2699 BP.
XX ADD22860;
AC
XX
XX 15-JAN-2004 (first entry)
DE Human full length cDNA encoding histamine H3 receptor.
XX
XX Human; ss; Histamine H3 receptor; GPCR; G protein-coupled receptor; gene;
KW depression; anxiety; schizophrenia; Parkinson's disease; obesity;
KW hypertension; Tourette's syndrome; sexual dysfunction; drug addiction;
KW drug abuse; cognitive disorder; Alzheimer's disease;
KW obsessive-compulsive behaviour; panic attack; pain; eating disorder;
KW anorexia; cardiovascular disorder; cerebrovascular disorder; diabetes;
KW constipation; arrhythmia; ulcer; asthma; allergy; inflammation;
KW prostate dysfunction.
XX
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 299..1636
FT /tag= a
FT /product= "Histamine H3 receptor"
XX
XX US6437100-B1.
XX
XX 20-ANG-2002.
XX
XX 21-ANG-2000; 2000US-00642514.
XX
XX 07-OCT-1998; 98US-00167354.
XX
XX (ORTH) ORTHO PHARM CORP.
XX
XX Lovenberg TW, Erlander M, Huvar A, Pyati J;
XX
XX WPI: 2003-810293/76.
XX
XX P-PSDB; ADD22854.
XX
XX
XX New antibody against human histamine H3 receptor, preferably with
PT receptor antagonist activity, useful for diagnostic purposes and for
PT treating diseases such as depression, Parkinson's disease, obesity or
PT hypertension.
XX
XX Example 1; SEQ ID NO 5; 25pp; English.
XX
XX The invention relates to a monospecific antibody immunologically reactive
CC with a protein appearing as ADD22854, where the protein functions as a
CC human histamine H3 receptor. The antibody blocks intracellular signaling
CC activity of the human histamine H3 receptor in response to ligand
CC binding. The antibody is useful for detecting and quantifying expression
CC of human histamine H3 receptors, which may be useful for diagnostic,
CC epidemiological or forensic purposes. The antibody is potentially useful
CC in treating diseases such as depression, anxiety, schizophrenia,
CC Parkinson's disease, obesity, hypertension, Tourette's syndrome, sexual
CC dysfunction, drug addiction or drug abuse, cognitive disorders, sexual
CC Alzheimer's disease, obsessive-compulsive behaviour, panic attacks, pain,
CC eating disorders and anorexia, cardiovascular and cerebrovascular
CC disorders, diabetes, constipation, arrhythmia, ulcers, asthma, allergy,
CC inflammation, or prostate dysfunction. The present sequence is the full
CC length cDNA encoding the histamine H3 receptor.
XX
XX Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 2699; DB 10; Length 2699;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAACGCTCCGCGGTGACACCGGCTGACAGGCTCCGCGCTCTCC 60
DB 1 CCAACGCTCCGCGGTGACACCGGCTGACAGGCTCCGCGCTCTCC 60
QY 61 GCTGACGACGCGCGCTGCGACCTGAGCTCGGATCCGACCCCGCTCGCA 120
DB 61 GCTGACGACGCGCGCTGCGACCTGAGCTCGGATCCGACCCCGCTCGCA 120
QY 121 CGGCTGCTTGAAGCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 CGGCTGCTTGAAGCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 ACCCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 181 ACCCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 241 CCCAGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 241 CCCAGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 GGAAGCG 360
DB 301 GGAAGCG 360
QY 361 GCG 420
DB 361 GCG 420
QY 421 GCGCGCTGCTCATGCTGACGACGCGCGCGCGCGCGCGCGCGCGCG 480
DB 421 GCGCGCTGCTCATGCTGACGACGCGCGCGCGCGCGCGCGCGCGCG 480
QY 481 CGAATCGAGCTTCGCGACCGCAAGCACTTCTTCTGCTGCAACTTCG 540
DB 481 CGAATCGAGCTTCGCGACCGCAAGCACTTCTTCTGCTGCAACTTCG 540
QY 541 CCTGCTGCGCGCGCTTCTGATCCCACTGATGATCCCACTGATGATCC 600
DB 541 CCTGCTGCGCGCGCTTCTGATCCCACTGATGATCCCACTGATGATCC 600
QY 601 CTTGCGCGCGCGCGCTTCTGATGATGATGATGATGATGATGATGAT 660
DB 601 CTTGCGCGCGCGCGCTTCTGATGATGATGATGATGATGATGATGAT 660
QY 661 TGCCTTCAACATGCTGCTCATGACTGACGCGCTTCTGCTGCTGCTG 720
DB 661 TGCCTTCAACATGCTGCTCATGACTGACGCGCTTCTGCTGCTGCTG 720
QY 721 ATACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
DB 721 ATACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 781 GCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 781 GCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 CTCATCCCGCGAGGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 841 CTCATCCCGCGAGGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 GGTTCACACCTGAGATCTTAAAGCGCTTCTGAGCGCTGCTTAACTG 960
DB 901 GGTTCACACCTGAGATCTTAAAGCGCTTCTGAGCGCTGCTTAACTG 960
QY 961 CTAACGGAATTCAGAGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTG 1020
DB 961 CTAACGGAATTCAGAGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1021 CCCGAGCCCGCTCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080

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Db 1021 CCCGAGCCCTCCGAGGCCAGGCTCTACACCTCCACCGCTGTGCTGCGGCTG 1080
Qy 1081 CTGGCAGAAAGGGGCAAGGGAGGCAATGCCGTGTCACAGATATGGGTGGTGAAGGCGC 1140
Db 1081 CTGGCAGAAAGGGGCAAGGGAGGCAATGCCGTGTCACAGATATGGGTGGTGAAGGCGC 1140
Qy 1141 CGTAGGCGCTGAGGGCGGGGAGGCGACCTCGGGGGGTGGCGGTGGGGGCGGCTCGGTGGC 1200
Db 1141 CGTAGGCGCTGAGGGCGGGGAGGCGACCTCGGGGGGTGGCGGTGGGGGCGGCTCGGTGGC 1200
Qy 1201 TTCACCACTCCAGCTCCGAGCACTCTCTGAGAGGCACTGAGAGGCGCGCTCACTCAA 1260
Db 1201 TTCACCACTCCAGCTCCGAGCACTCTCTGAGAGGCACTGAGAGGCGCGCTCACTCAA 1260
Qy 1261 GAGGGGCTCCAGAGCCGTGGCGCTCTGGCGCTCTGGAGAGAGCGCATGAAATGGTGTG 1320
Db 1261 GAGGGGCTCCAGAGCCGTGGCGCTCTGGCGCTCTGGAGAGAGCGCATGAAATGGTGTG 1320
Qy 1321 CCAGAGCTTCAACCAAGCGCTTTGGGTGTCTCGGGACAGAGAAATGGCCAAATCGCTGGC 1380
Db 1321 CCAGAGCTTCAACCAAGCGCTTTGGGTGTCTCGGGACAGAGAAATGGCCAAATCGCTGGC 1380
Qy 1381 CGTCATCGTAGAGCATTTTGGGCTCTGCTGAGGCCCCATACACGCTGTGATGATCAATCG 1440
Db 1381 CGTCATCGTAGAGCATTTTGGGCTCTGCTGAGGCCCCATACACGCTGTGATGATCAATCG 1440
Qy 1441 GGCCTGCTCATAGGCACTGAGCGCTCCCTGACTACTGTAGAGAACTCTCTTGTGGCTCT 1500
Db 1441 GGCCTGCTCATAGGCACTGAGCGCTCCCTGACTACTGTAGAGAACTCTCTTGTGGCTCT 1500
Qy 1501 GTGGGCAACTCGGCTGTCAACCTGTCTTACCTCTGTGCAACACAGCTTCCGCGC 1560
Db 1501 GTGGGCAACTCGGCTGTCAACCTGTCTTACCTCTGTGCAACACAGCTTCCGCGC 1560
Qy 1561 GGCCTTCAACCAAGCTCTGAGGCCCCAGAGAGCTCAAAATCGAGCCCAAGCTCCCTGGA 1620
Db 1561 GGCCTTCAACCAAGCTCTGAGGCCCCAGAGAGCTCAAAATCGAGCCCAAGCTCCCTGGA 1620
Qy 1621 GCACTGCTGAGAAATGAGTGGCCCAAGAGAGCTCCCTCAGCCAGCGCTCTCTAGCCAG 1680
Db 1621 GCACTGCTGAGAAATGAGTGGCCCAAGAGAGCTCCCTCAGCCAGCGCTCTCTAGCCAG 1680
Qy 1681 GTCTCTGGGCACTGTGGCCCTGTGCTGCCCTTACCCGAGCTGTTCCTCCAGGGGTGAGCC 1740
Db 1681 GTCTCTGGGCACTGTGGCCCTGTGCTGCCCTTACCCGAGCTGTTCCTCCAGGGGTGAGCC 1740
Qy 1741 CGCGGTGTGTGGCCCTCTCTTAATGCAAGGAGAGCACTGAGAGGCGGCTTC 1800
Db 1741 CGCGGTGTGTGGCCCTCTCTTAATGCAAGGAGAGCACTGAGAGGCGGCTTC 1800
Qy 1801 CTGGGTTTGGCAGAGGGGCCCTCACTGTGCTGAGACTGAGAGGCTGGGCGCTGCGCC 1860
Db 1801 CTGGGTTTGGCAGAGGGGCCCTCACTGTGCTGAGACTGAGAGGCTGGGCGCTGCGCC 1860
Qy 1861 CCCACATTTGCTGCTCAACCGGGAGAGGACAGTGTGAGGTCCAGACATCTGCCACCC 1920
Db 1861 CCCACATTTGCTGCTCAACCGGGAGAGGACAGTGTGAGGTCCAGACATCTGCCACCC 1920
Qy 1921 CCGTGTGTGTGGCCAGCTTGTGAGTTACTGTGTGTGTGTCTTCCAAAGAGACACTGTG 1980
Db 1921 CCGTGTGTGTGGCCAGCTTGTGAGTTACTGTGTGTGTGTCTTCCAAAGAGACACTGTG 1980
Qy 1981 GTGTGTCTCAGAGCTTGTGCTTGTGAGATTTGTGCTGCAAGTGAACACTGACACC 2040
Db 1981 GTGTGTCTCAGAGCTTGTGCTTGTGAGATTTGTGCTGCAAGTGAACACTGACACC 2040
Qy 2041 CCGTGTGTGTGCACTGCAACCGTCTCTTCCCGAGCAAGGCGAGACACTGCTTGTGCTG 2100
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Qy 2101 CCTTGTGTCTCTGTGATTAAGCTCAGGCGTGGCCCTTTCACCCCTTCCCAACAACCTCT 2160
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Db 2101 CCTTGTGTCTCTGTGATTAAGCTCAGGCGTGGCCCTTTCACCCCTTCCCAACAACCTCT 2160
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Qy 2221 TTTGGGTGTCTTCAAGAAATGAAAGAAACATGTCTGTGAACTTGAATGTTGCGGG 2280
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Qy 2281 ATGTTAATCAAGAGACAAATTTGCTGAGAGCTCAGGGCTGAAATGGCAGGTGGG 2340
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Db 2341 CTCCACGCGCTCTCTCTCTCCCTTAAGGCTTCCGGGTGAGCTTGTGCAAGTGTCTGCC 2400
Qy 2401 CACCCGCGCTGTGGGCTCACACAGGCGCTGTGAGGCTGAGGCTGCGCGGCACTGTGTT 2460
Db 2401 CACCCGCGCTGTGGGCTCACACAGGCGCTGTGAGGCTGAGGCTGCGCGGCACTGTGTT 2460
Qy 2461 GCTCACCAGAGACCTCTGAGGAGTGTGTGGAGAGAGGGGCGCGGCTGTGGCCAGAGGTC 2520
Db 2461 GCTCACCAGAGACCTCTGAGGAGTGTGTGGAGAGAGGGGCGCGGCTGTGGCCAGAGGTC 2520
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Db 2521 CAAAGGCTGAGAGGGGCGGTTCAGAGAGAGTCCCGGCGAGGGGCGCTTGTGCAATGTGCT 2580
Qy 2581 GTGCAACCGGCGCAGCGGCTCTGATGCTCTGTGCTGTGAGGCGGCTGAGGCTGCGCA 2640
Db 2581 GTGCAACCGGCGCAGCGGCTCTGATGCTCTGTGCTGTGAGGCGGCTGAGGCTGCGCA 2640
Qy 2641 AACCGTAGGTCACAAATTAAGTATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT 2699
Db 2641 AACCGTAGGTCACAAATTAAGTATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT 2699

RESULT 7
AD089179
ID AD089179 standard; cdna; 2699 BP.
XX
AC AD089179;
XX
XX 21-OCT-2004 (first entry)
XX
DE Human urological disorder related protein 8203 encoding cdna SEQ.131.
XX
KW urological disorder; uropathic; cytosstatic; urinary incontinence;
KW benign prostatic hyperplasia; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 299..1636
FT /tag= a
FT /product= "urological disorder related protein 8203"
XX
PN MO2004065576-A2.
XX
PD 05-AUG-2004.
XX
PF 14-JAN-2004; 2004MO-US000750.
XX
PR 15-JAN-2003; 2003US-0440318P.
PR 04-FEB-2003; 2003US-0444783P.
PR 27-MAR-2003; 2003US-0457901P.
PR 08-MAY-2003; 2003US-0468775P.
PR 19-MAY-2003; 2003US-0471614P.
PR 16-JUN-2003; 2003US-0478742P.
PR 18-JUL-2003; 2003US-0488529P.
PR 30-JUL-2003; 2003US-0491156P.
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QY	1621	GCACGTCTGGAAGAGATGGAGGCGCACACAGAGCTCCCTCAGCAGAGCTCTCTCAAGCCAG	1680
Dp	1621	GCACGTCTGGAAGATGATGGAGCCACACAGAGCTCCCTCAGCAGAGCTCTCTCAAGCCAG	1680
QY	1681	GTCCTCTGGGCAATCGAGCCCTGCTGAGCCCTCAACCGAGCTCGTTGCCCCAGAGGGATGAGCC	1740
Dp	1681	GTCCTCTGGGCAATCGAGCCCTGCTGAGCCCTCAACCGAGCTCGTTGCCCCAGAGGGATGAGCC	1740
QY	1741	CGCGGTGTCTGTGGACCCCTCTTAATGCAACGAGACCACTTCGCATGAGAGCGCTTC	1800
Dp	1741	CGCGGTGTCTGTGGACCCCTCTTAATGCAACGAGACCACTTCGCATGAGAGCGCTTC	1800
QY	1801	CTGGGTTGGCCAGAGAGGAGCCCTCACTGGCTAGACTGAGAGGTGGGTGGCCGCTGACC	1860
Dp	1801	CTGGGTTGGCCAGAGAGGAGCCCTCACTGGCTAGACTGAGAGGTGGGTGGCCGCTGACC	1860
QY	1861	CCCAACATTTCTGGCTCCACACGGGAGAGGACACTGTGAGAGTCCCAAGACATGTGCGCCACC	1920
Dp	1861	CCCAACATTTCTGGCTCCACACGGGAGAGGACACTGTGAGAGTCCCAAGACATGTGCGCCACC	1920
QY	1921	CTGTCTGGTGGCCACCCCTTGCACTTACTGAGTGTGTTCTTCCAAAGCAAGACCTGG	1980
Dp	1921	CTGTCTGGTGGCCACCCCTTGCACTTACTGAGTGTGTTCTTCCAAAGCAAGACCTGG	1980
QY	1981	GTCGTCTCAGAGCTTCTGAGCCCTAGCAAGTTGCTCTGACAGTGCACACCTGCACACC	2040
Dp	1981	GTCGTCTCAGAGCTTCTGAGCCCTAGCAAGTTGCTCTGACAGTGCACACCTGCACACC	2040
QY	2041	CCCTGACACACACTGACACACCGTCCCTCCCGGAGAAAGCCCAAGACACTGCGCTTGTG	2100
Dp	2041	CCCTGACACACACTGACACACCGTCCCTCCCGGAGAAAGCCCAAGACACTGCGCTTGTG	2100
QY	2101	CCCTCTGTCTCTTGCATTAAGCTCAGAGCTGAGCCCTTTCACCCCTCTTCCACCAACTCT	2160
Dp	2101	CCCTCTGTCTCTTGCATTAAGCTCAGAGCTGAGCCCTTTCACCCCTCTTCCACCAACTCT	2160
QY	2161	CTCTGCCCCCAAAAGTGTCAAGGGGAGCCCTAGGAACCTGGAAGCTGTCTGCTTTTCCA	2220
Dp	2161	CTCTGCCCCCAAAAGTGTCAAGGGGAGCCCTAGGAACCTGGAAGCTGTCTGCTTTTCCA	2220
QY	2221	TTCTGGGTGTCTTCAAGAAAGATGAAGAAAGAAACAATGTCTGTGAACTTGAATGTTCTGGG	2280
Dp	2221	TTCTGGGTGTCTTCAAGAAAGATGAAGAAAGAAACAATGTCTGTGAACTTGAATGTTCTGGG	2280
QY	2281	ATGTTTAAATCAAGAGAGACAAATATTCGTAGAGAGCTCAGAGGCTGAAATTTGCAAGGTGGG	2340
Dp	2281	ATGTTTAAATCAAGAGAGACAAATATTCGTAGAGAGCTCAGAGGCTGAAATTTGCAAGGTGGG	2340
QY	2341	CTCCACAGCCCTCTCCCTCCGCTTAAGGCTTCCGGCTGAGCTGTGACCAAGCTCTTGCC	2400
Dp	2341	CTCCACAGCCCTCTCCCTCCGCTTAAGGCTTCCGGCTGAGCTGTGACCAAGCTCTTGCC	2400
QY	2401	CACCCCGCTCTGGGCTCACACACAGCCCTGTGTGCCAAAGCTGTGCCGCGACACTCTGTTT	2460
Dp	2401	CACCCCGCTCTGGGCTCACACACAGCCCTGTGTGCCAAAGCTGTGCCGCGACACTCTGTTT	2460
QY	2461	GCTCACCACGAGACCTCTGGGGGTGTGTTGGAGAGAGGGGAGCCCGGCTGGGAGCCGAGGGTCC	2520
Dp	2461	GCTCACCACGAGACCTCTGGGGGTGTGTTGGAGAGAGGGGAGCCCGGCTGGGAGGGTCC	2520
QY	2521	CAAAGCGGTGCAGGGGCGGTCCAGAGAGAGTCCCGGAGAGGGGCGCGTGTGCATGTGCT	2580
Dp	2521	CAAAGCGGTGCAGGGGCGGTCCAGAGAGAGTCCCGGAGAGGGGCGCGTGTGCATGTGCT	2580
QY	2581	GTCGACCCGTGECACAGCGCTCTGCATGTCTCTGTGCGTGTGECGCGCTGCGCTCTGCA	2640
Dp	2581	GTCGACCCGTGECACAGCGCTCTGCATGTCTCTGTGCGTGTGECGCGCTGCGCTCTGCA	2640
QY	2641	AAACGTGAGGTCAACAATAAGTAAATTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2699
Dp	2641	AAACGTGAGGTCAACAATAAGTAAATTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2699

[illegible]

OY	181	ACCCGACCCCGGACAAAGGCGCCGCAAAAGACAGAGCTCCCGGGCCCGGGGCGCTCCCGGGCG	240
Db	181	ACCGGACCCCGGACAAAGGCGCCGCAAAAGACAGAGCTCCCGGGCCCGGGGCGCTCCCGGGCG	240
OY	241	CCGAGCTCTCGAGCGGGCGCGCTGCGCCCGCATCCCGGAGCGCGGTAGCGCTGCGGGCCAT	300
Db	241	CCGAGCTCTCGAGCGGGCGCGCTGCGCCCGCATCCCGGAGCGCGGTAGCGCTGCGGGCCAT	300
OY	301	GGAGCGCGCGCGCGCCCGGACGGGCGCTTACAGCTTCGGGGGCGCTGGGGGGCGATGCGGC	360
Db	301	GGAGCGCGCGCGCGCCCGGACGGGCGCTTACAGCTTCGGGGGCGCTGGGGGGCGATGCGGC	360
OY	361	GGCGGCGGGCGGGGCGCGCGGCTTCTCGCGGACGCTGACCCGCGGTGCTGGCGCGGCTCAT	420
Db	361	GGCGGCGGGCGGGGCGCGCGGCTTCTCGCGGACGCTGACCCGCGGTGCTGGCGCGGCTCAT	420
OY	421	GGCGCTGCTCATTCGTGGCCACGGTGCTGGGCAACGCGCTGGTCATGCTCGCTTCGTGGC	480
Db	421	GGCGCTGCTCATTCGTGGCCACGGTGCTGGGCAACGCGCTGGTCATGCTCGCTTCGTGGC	480
OY	481	GGAETCGAGCGCTCGGACCAACGAACAACTTCCTCGTCAACCTCGGCATCTCCGACTT	540
Db	481	GGAETCGAGCGCTCGGACCAACGAACAACTTCCTCGTCAACCTCGGCATCTCCGACTT	540
OY	541	CCTCGTCGGCGCCTTCTGTCATCCCACTGATATACCTTACGCTGTGACAGGCGCGCTGGAC	600
Db	541	CCTCGTCGGCGCCTTCTGTCATCCCACTGATATACCTTACGCTGTGACAGGCGCGCTGGAC	600
OY	601	CTTGCGGCGGGGCGCTCTGCAAGCTGTGGCTGGTAGTGAATACTGCTGTGACACTCTCTC	660
Db	601	CTTGCGGCGGGGCGCTCTGCAAGCTGTGGCTGGTAGTGAATACTGCTGTGACACTCTCTC	660
OY	661	TGCGCTTCAACATCGTGCTCATCAGCTACGACGAGCTTCGTGCGGTGACCCGAGCGGCTTC	720
Db	661	TGCGCTTCAACATCGTGCTCATCAGCTACGACGAGCTTCGTGCGGTGACCCGAGCGGCTTC	720
OY	721	ATACCGGGGCCGACGAGGCTGAACGCGGCGGACAGTCGGAAGATGCTGCTGGTGCGGT	780
Db	721	ATACCGGGGCCGACGAGGCTGAACGCGGCGGACAGTCGGAAGATGCTGCTGGTGCGGT	780
OY	781	GCTGGCGCTTCGTCGTGACGAGACGAGCATCTGAGCTGGGAGATACCTGTGCGGGGGGAG	840
Db	781	GCTGGCGCTTCGTCGTGACGAGACGAGCATCTGAGCTGGGAGATACCTGTGCGGGGGGAG	840
OY	841	CTCATCCCGAGGGGCACTGCTATGCGAGTCTTCTTACACTGGTACTTCTCATCAC	900
Db	841	CTCATCCCGAGGGGCACTGCTATGCGAGTCTTCTTACACTGGTACTTCTCATCAC	900
OY	901	GGCTTCCACCTCGAGTCTTATAAGCCTTCTCTAGGCTCACTTCTTAACTCTAGAT	960
Db	901	GGCTTCCACCTCGAGTCTTATAAGCCTTCTCTAGGCTCACTTCTTAACTCTAGAT	960
OY	961	CTACTGTAACATCCAGAGGCGCACCGGCTCGGTGATGGGGCTCAGAGGACGCGG	1020
Db	961	CTACTGTAACATCCAGAGGCGCACCGGCTCGGTGATGGGGCTCAGAGGACGCGG	1020
OY	1021	CCCGGAGCTCCCTCCGAGGCCAGGCTCTACACACCCCAACCGCTGGCTGCTGGGCTG	1080
Db	1021	CCCGGAGCTCCCTCCGAGGCCAGGCTCTACACACCCCAACCGCTGGCTGCTGGGCTG	1080
OY	1081	CTGGCAGAAAGGGGACAGGGGAGGCCATACCGCTGCAAGGTATGGGATGGGTAAGGCGGC	1140
Db	1081	CTGGCAGAAAGGGGACAGGGGAGGCCATACCGCTGCAAGGTATGGGATGGGTAAGGCGGC	1140
OY	1141	CGTAGGCGCTGAGGCGGGGAGGCGACCTTCGGGGGTGGCGGTGGGCGGCTCGTGGC	1200
Db	1141	CGTAGGCGCTGAGGCGGGGAGGCGACCTTCGGGGGTGGCGGTGGGCGGCTCGTGGC	1200
OY	1201	TTTCAATCCACTTCAGCTCCGGGAGCTCTCTCGAGGGGACCTAGAGAGCGCGCTCATCTAA	1260
Db	1201	TTTCAATCCACTTCAGCTCCGGGAGCTCTCTCGAGGGGACCTAGAGAGCGCGCTCATCTAA	1260

QY	1261	GAGGGGCTCCAAAGCGCTCGGCTCTCGGCGCTGCTGAGAAAGGCAATGAAGATGCTC	1320
Db	1261	GAGGGGCTCCAAAGCGCTCGGCGCTCTCGGCGCTGCTGAGAAAGGCAATGAAGATGCTC	1320
QY	1321	CCAGAGCTTCAACCAAGCGCTTTCGGCTGTCTCGGGAACGAAAGTGGCCAAATCGCTGGC	1380
Db	1321	CCAGAGCTTCAACCAAGCGCTTTCGGCTGTCTCGGGAACGAAAGTGGCCAAATCGCTGGC	1380
QY	1381	CGTCATCGTGAACAATCTTTGGGGCTCTGCTGGGGCCCAATACAGCTGCTGATGATCATCCG	1440
Db	1381	CGTCATCGTGAACAATCTTTGGGGCTCTGCTGGGGCCCAATACAGCTGCTGATGATCATCCG	1440
QY	1441	GGCGGCGCTGCAATGGCACTGCGGCTCGGCCGATCATGGTAAGAAACCTCTTGGGCTCCT	1500
Db	1441	GGCGGCGCTGCAATGGCACTGCGGCTCGGCCGATCATGGTAAGAAACCTCTTGGGCTCCT	1500
QY	1501	GTVGGGCCAACTCGGCTGTCAACCCCTGTCTCTTACCTCTGTGCCACCAAGCTTCGCGCG	1560
Db	1501	GTVGGGCCAACTCGGCTGTCAACCCCTGTCTCTTACCTCTGTGCCACCAAGCTTCGCGCG	1560
QY	1561	GGCCTTCAACAAGCTGCTCTGCCCCCAGAAAGCTCAAAATCCAGCCCAAGCTCCCTGA	1620
Db	1561	GGCCTTCAACAAGCTGCTCTGCCCCCAGAAAGCTCAAAATCCAGCCCAAGCTCCCTGA	1620
QY	1621	GCACTGCTGGAAGTGAATGAGTGGGCCCAACAAGGCTCCCTCAGCAGAGCTCTCTACGCCAG	1680
Db	1621	GCACTGCTGGAAGTGAATGAGTGGGCCCAACAAGGCTCCCTCAGCAGAGCTCTCTACGCCAG	1680
QY	1681	GTCCTCTGGGCAATCTGGGCCCTGTGCCCCCTACCCGAGCTGTTCCCCAGGGGTGAAGCC	1740
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QY	1741	CGCGGTGCTGTGGCCCTCTCTTAATGCAACGAGGCAACCCCTGCAATGAGAGCGCCTTC	1800
Db	1741	CGCGGTGCTGTGGCCCTCTCTTAATGCAACGAGGCAACCCCTGCAATGAGAGCGCCTTC	1800
QY	1801	CTGGGTTTGGCCAGAGGGGCCCTCACTGAGCTGGAATGAGAGGCTGGGTGGCGGCTTGGCC	1860
Db	1801	CTGGGTTTGGCCAGAGGGGCCCTCACTGAGCTGGAATGAGAGGCTGGGTGGCGGCTTGGCC	1860
QY	1861	CCCAATCTGGGCTCAACCGGGAGAGGGAAGTCTGGAAGGTCCAGACATGCTGGCCACC	1920
Db	1861	CCCAATCTGGGCTCAACCGGGAGAGGGAAGTCTGGAAGGTCCAGACATGCTGGCCACC	1920
QY	1921	CCTGCTGTGGCCAACCTTTCGCACTTACCTGTGGTGTCTTTCGCAAGCAAGCACTTGG	1980
Db	1921	CCTGCTGTGGCCAACCTTTCGCACTTACCTGTGGTGTCTTTCGCAAGCAAGCACTTGG	1980
QY	1981	GTCGTCTCAAGGCTTCTGTGCTTACGAGTTTGTCTGTGACATGTGCACACCTGCAACC	2040
Db	1981	GTCGTCTCAAGGCTTCTGTGCTTACGAGTTTGTCTGTGACATGTGTGCACACCTGCAACC	2040
QY	2041	CCTGCAACAACCTGCAACCGTCCCTCCCGGACAAAGCCAGAGACATGCTCTTGGCTG	2100
Db	2041	CCTGCAACAACCTGCAACCGTCCCTCCCGGACAAAGCCAGAGACATGCTCTTGGCTG	2100
QY	2101	CCTTCTGTCTCTTGCATTAAGCTCAAGGCTTGGCCCTTTCACCCCTTTCGCCACCAACTCT	2160
Db	2101	CCTTCTGTCTCTTGCATTAAGCTCAAGGCTTGGCCCTTTCACCCCTTTCGCCACCAACTCT	2160
QY	2161	CTGTGCCCAAAAGTGTCAAGGGGCGCTGAGAACTCGAAAGCTGTCTCGCTTTTCCA	2220
Db	2161	CTGTGCCCAAAAGTGTCAAGGGGCGCTGAGAACTCGAAAGCTGTCTCGCTTTTCCA	2220
QY	2221	TTTCGGGGTTTTTCAAGAAAGTGAAGAAAGAAACATGTCTGTGAATTTGAATTTTCGGGG	2280
Db	2221	TTTCGGGGTTTTTCAAGAAAGTGAAGAAAGAAACATGTCTGTGAATTTGAATTTTCGGGG	2280
QY	2281	ATGTTTAATCAAGAGAGCAAAATTGCTGAGAGAGCTCAGGGCTGGAATTTGCAGAGTGTGGG	2340
Db	2281	ATGTTTAATCAAGAGAGCAAAATTGCTGAGAGAGCTCAGGGCTGGAATTTGCAGAGTGTGGG	2340
QY	2341	CTCCACGCGCTCTCCCTCCGCTAAGGCTTCGGCTGAGCTGTGCCAGCTGCTTTCGCC	2400

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Db 2341 CTCGCAAGCCCTCTCCCTCCGTAAGGCTCCGGCTGAGCTGTGCGAGCTGCTTCC 2400
Qy 2401 CACCCCGCTCTGGGCTCACACAGCCCTGTGGCCAAAGCTCCCGGCACTGTGTTT 2460
Db 2401 CACCCCGCTCTGGGCTCACACAGCCCTGTGGCCAAAGCTCCCGGCACTGTGTTT 2460
Qy 2461 GCTCACCAGGACCTCTGGGGGTTGTTGGAGAGAGGGGGCCGGCTGGGCGAGGGTCC 2520
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Qy 2581 GTGACACCCGTGACACGGGCTGTGACATGCTCTCTGCTGTGGCCGCTGCGCTGCA 2640
Db 2581 GTGACACCCGTGACACGGGCTGTGACATGCTCTCTGCTGTGGCCGCTGCGCTGCA 2640
Qy 2641 AACCGAGGTCACATTAAGTATTTTAAAAAATAAAAAAATAAAAAA 2699
Db 2641 AACCGAGGTCACATTAAGTATTTTAAAAAATAAAAAAATAAAAAA 2699

RESULT 9
AAx02885
ID AAx02885 standard; cDNA; 2689 BP.
XX
AC AAx02885;
XX
DT 17-MAY-1999 (first entry)
XX
DE Human mAChR-6 cDNA.
XX
KW mAChR-6; muscarinic acetylcholine receptor 6; disorder; secretion;
KW acetylcholine responsive cell; phosphatidylinositol turn-over;
KW smooth muscle cell contraction; nervous system disorder; glandular;
KW schizo-effective disorder; affective disorder; sleep disorder;
KW movement disorder; eating disorder; drinking disorder; human; 89.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 291..1628
FT /*tag= a
FT /product= "mAChR-6"
XX
PN US5882893-A.
XX
PD 16-MAR-1999.
XX
PF 04-DEC-1997; 97US-00985090.
XX
PR 04-DEC-1997; 97US-00985090.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Goodearl AD;
XX
DR WPI; 1999-214063/18.
XX
DR P-PSDB; AAW92975.
XX
PT Nucleic acids encoding muscarinic acetylcholine receptor 6 - useful for
PT modulating the effects of acetylcholine on acetylcholine responsive
PT cells.
XX
PS Claim 2j; Fig 1A-D; 59pp; English.
XX
CC This invention describes the isolation of a novel human muscarinic
CC acetylcholine receptor 6 (mAChR-6), capable of modulating the effects of
CC acetylcholine on acetylcholine responsive cells. mAChR-6 cDNAs and
CC polypeptides may be used to detect naturally occurring mutations of the
CC mAChR-6 gene and determine if a subject with the mutated gene is at risk

CC of (or is predisposed to have) a mAChR-6 related disorder, modulate cell
CC activity mediated by mAChR-6 (e.g. biological processes mediated by
CC phosphatidylinositol turn-over and signalling), secretion of a molecule
CC (e.g. a neurotransmitter or a glandular enzyme), or contraction of a
CC smooth muscle cell, treat disorders mediated by abnormal mAChR-6 activity
CC e.g. nervous system disorders (e.g. amnesia, apraxia, agnosia, amnesic
CC dysnomia), amnesia, amnesia, amnesia, amnesia, amnesia, amnesia,
CC Alzheimer's related memory loss and learning disability, visual
CC hallucinations, perceptual disturbances, and Lewy body dementia
CC associated delirium), schizo-effective disorders (e.g. schizophrenia with
CC mood swings, and depressive illness), affective disorders, sleep
CC disorders (e.g. REM sleep abnormalities, paradoxical sleep abnormalities,
CC sleep-wakefulness, and body temperature or respiratory depression
CC abnormalities during sleep), pain generating mechanism disorders (e.g.
CC related to irritable bowel syndrome (IBS), or chest pain), movement
CC disorders (e.g. related to Parkinson's disease), eating disorders (e.g.
CC insulin hypersecretion related obesity), drinking disorders (e.g.
CC diabetic polydipsia), smooth muscle related disorders (e.g. IBS,
CC diverticular disease, urinary incontinence, oesophageal achalasia, and
CC chronic obstructive airways disease), cardiac disorders (e.g. pathologic
CC bradycardia or tachycardia, arrhythmia, flutter and fibrillation), and
CC glandular disorders (e.g. xerostomia and diabetes mellitus)

XX
SQ Sequence 2689 BP; 393 A; 990 C; 806 G; 500 T; 0 U; 0 Other;

Query Match 97.6%; Score 2635.2; DB 2; Length 2689;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

Qy 25 CGACCGGACGCGGCTCAGGCTCCGGCTCTCCCGCTGACAGCGCGGCTCCGGCC 84
Db 18 CGACCGGACGCGGCTCAGGCTCCGGCTCTCCCGCTGACAGCGCGGCTCCGGCC 77
Qy 85 CCACTGAGCTCGGATCCGGCCCGGCTCCGGCACCGCTGCTGAGTCCCGGCGCCG 144
Db 78 CCACTGAGCTCGGATCCGGCCCGGCTCCGGCACCGCTGCTGAGTCCCGGCGCCG 137
Qy 145 GCGCCCGGACCAATGCGTGGGGGCGCCCGAGGGGAAACCGACCGGCGCAAGGGCCGCA 204
Db 138 GCGCCCGGACCAATGCGTGGGGGCGCCCGAGGGG-AAACCGACCGGCGCAAGGGCCGCA 196
Qy 205 AAGACGAGGCTCCGGGCGGCGGCGCCCTCCGGGCGCCGCACTCTGAGCGCGGCTTCG 264
Db 197 AAGACGAGGCTCCGGGCGGCGGCGCCCTCCGGGCGCCGCACTCTGAGCGCGGCTTCG 256
Qy 265 CCGCGCTCCCGAGCGCGCTGAGCTTCGGGGGCGCATAGAGCGCGCGCCGCAAGGGCC 324
Db 257 CCGCGCTCCCGAGCGCGCTGAGCTTCGGGGGCGCATAGAGCGCGCGCGCGCAAGGGCC 316
Qy 325 GCTGAACGCTTCGGGGGCGCTGCGCGGCGCATAGCGCGCGCGCGCGCGCGCTT 384
Db 317 GCTGAACGCTTCGGGGGCGCTGCGCGGCGCATAGCGCGCGCGCGCGCGCGCTT 376
Qy 385 CTCGGAGCTTGAGACCGCGGCTGCGCGGCGCATAGCGCGCTCTGATGCGGCGCAAGGT 444
Db 377 CTCGGAGCTTGAGACCGCGGCTGCGCGGCGCATAGCGCGCTCTGATGCGGCGCAAGGT 436
Qy 445 GCTGGGCAACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504
Db 437 GCTGGGCAACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496
Qy 505 CAATCTTCTTCGCTGCACTGCTGCACTGCTGCACTGCTGCACTGCTGCACTGCTGCA 564
Db 497 CAATCTTCTTCGCTGCACTGCTGCACTGCTGCACTGCTGCACTGCTGCACTGCTGCA 556
Qy 565 ACTGATGTAACCTTACGCTGCAAGCGCGCTGCAAGCTTCCGCGGCGCTTCCGAGCT 624
Db 557 ACTGATGTAACCTTACGCTGCAAGCGCGCTGCAAGCTTCCGCGGCGCTTCCGAGCT 616
Qy 625 GTGGCTGTAAGTGAATCACTGCTGCACTGCTGCACTGCTGCACTGCTGCACTGCTGCA 684
Db 617 GTGGCTGTAAGTGAATCACTGCTGCACTGCTGCACTGCTGCACTGCTGCACTGCTGCA 676

QY 685 CTAAGACCGCTTCTGTGGTCAACCCGAGCGTCTCATACCGGGCCACAGAGGTGACAC 744
DB 677 CTAAGACCGCTTCTGTGGTCAACCCGAGCGTCTCATACCGGGCCACAGAGGTGACAC 736
QY 745 GCGGCGGGGAGTGGGGAAGATGCTGTGGTGTGGGTGTGGCCCTTCTGTGTGACAGAC 804
DB 737 GCGGCGGGGAGTGGGGAAGATGCTGTGGTGTGGGTGTGGCCCTTCTGTGTGACAGAC 796
QY 805 AACCATCTGAGTGGGAGTACCTGTCCGGGGGCACTCCATCCCGAGGGCCACTGTCTA 864
DB 797 AAGCATCTGAGTGGGAGTACCTGTCCGGGGGCACTCCATCCCGAGGGCCACTGTCTA 856
QY 865 TGGCGAGTTCTTCTAACAATGTAATCTTCTCATACGAGCTTCCAGCTTGAAGTTCTTAC 924
DB 857 TGGCGAGTTCTTCTAACAATGTAATCTTCTCATACGAGCTTCCAGCTTGAAGTTCTTAC 916
QY 925 GGCCTTCTCAGAGTCACTTCTTAACCTCAGACATCTACCTGAATCAGAGGGGAC 984
DB 917 GGCCTTCTCAGAGTCACTTCTTAACCTCAGACATCTACCTGAATCAGAGGGGAC 976
QY 985 CCGGCTTCGGGCTGGATGGGGCTTGAAGGAGCGCGGCCCGGACCCCTTCCGAGGCCA 1044
DB 977 CCGGCTTCGGGCTGGATGGGGCTTGAAGGAGCGCGGCCCGGACCCCTTCCGAGGCCA 1036
QY 1045 GGCCTTCAACCCCGCACCGCTGTGGTGTGGGCTGTGGCAGAGAGGGGACGAGGAGC 1104
DB 1037 GGCCTTCAACCCCGCACCGCTGTGGTGTGGGCTGTGGCAGAGAGGGGACGAGGAGC 1096
QY 1105 CATGCGGCTGCAAGATGGGGTGGGTGAGGGGCGTGAAGGCGTGAAGGCGGGGAGGC 1164
DB 1097 CATGCGGCTGCAAGATGGGGTGGGTGAGGGGCGTGAAGGCGTGAAGGCGGGGAGGC 1156
QY 1165 GAACCTCGGGGGTGGCGGTGGGGCGGCTCCGTGCTTCAACCCACTCCAGCTCCGGCAG 1224
DB 1157 GAACCTCGGGGGTGGCGGTGGGGCGGCTCCGTGCTTCAACCCACTCCAGCTCCGGCAG 1216
QY 1225 CTCTCTGAGGGGCACTGAAGGCGCGCTTCAAGAGGGGCTTCAAGCGTCCGCGTTC 1284
DB 1217 CTCTCTGAGGGGCACTGAAGGCGCGCTTCAAGAGGGGCTTCAAGCGTCCGCGTTC 1276
QY 1285 CTCTCTGAGGGGCACTGAAGGCGCGCTTCAAGAGGGGCTTCAAGCGTCCGCGTTC 1344
DB 1277 CTCTCTGAGGGGCACTGAAGGCGCGCTTCAAGAGGGGCTTCAAGCGTCCGCGTTC 1336
QY 1345 GCTGTCTCGGAGCAGGAAAGTGGCCAGTGTGCGCTGATCGTAGAGATCTTTGGGCT 1404
DB 1337 GCTGTCTCGGAGCAGGAAAGTGGCCAGTGTGCGCTGATCGTAGAGATCTTTGGGCT 1396
QY 1405 CTGCTGGGGCCCATACACGCTGTGATGATCATCCGGGCGGCTGCAATGGCACTGGCT 1464
DB 1397 CTGCTGGGGCCCATACACGCTGTGATGATCATCCGGGCGGCTGCAATGGCACTGGCT 1456
QY 1465 CCTGTACTGTGTAGGAAACCTCTTGTGGTCTGTGGGCGCAACTCCGCTGTCAACC 1524
DB 1457 CCTGTACTGTGTAGGAAACCTCTTGTGGTCTGTGGGCGCAACTCCGCTGTCAACC 1516
QY 1525 TGTCTCTACCTCTGTGCAACCAAGCTTCCGCGGGCTTCAACCAAGTGTCTGCCC 1584
DB 1517 TGTCTCTACCTCTGTGCAACCAAGCTTCCGCGGGCTTCAACCAAGTGTCTGCCC 1576
QY 1585 CCAAGAGCTCAAAATCCAGCCCAAGCTTCCGAGCACTGCTGAAGTGAAGTGAAGCCCA 1644
DB 1577 CCAAGAGCTCAAAATCCAGCCCAAGCTTCCGAGCACTGCTGAAGTGAAGTGAAGCCCA 1636
QY 1645 CCAAGAGCTTCCCTCAACCAAGCTTCTTGAAGCCCAAGTCTCCGAGCACTTGGCCCTGCT 1704
DB 1637 CCAAGAGCTTCCCTCAACCAAGCTTCTTGAAGCCCAAGTCTCCGAGCACTTGGCCCTGCT 1696
QY 1705 GCGCCCTTACCCGGCTGTCTCCCGAGGGGTGAGCCCGCGTGTCTGTGGCCCTCTCTTA 1764
DB 1697 GCGCCCTTACCCGGCTGTCTCCCGAGGGGTGAGCCCGCGTGTCTGTGGCCCTCTCTTA 1756
QY 1765 ATGCAACGAGCAACCTGCAATGAGGCGCTTCTGTGGTGTGCGCAGAGGGCCCTCTCA 1824

DB 1757 ATGCCACGCAACCCCTGCAATGAGGCGCTTCTGTGGTGTGCAAGAGGCCCTCTCA 1816
QY 1825 CTGCTGTGACTGAGAGCTTGGGTGGCGGCGCTTGGCCCGCCCACTTGTGCTCCAGGGGA 1884
DB 1817 CTGCTGTGACTGAGAGCTTGGGTGGCGGCGCTTGGCCCGCCCACTTGTGCTCCAGGGA 1875
QY 1885 GGAAGAGTGTGAGAGTCCGAGCATGTGCGCAACCCCTGCTGTGTGCCAACCCTTGCAG 1944
DB 1876 GGAAGAGTGTGAGAGTCCGAGCATGTGCGCAACCCCTGCTGTGTGCCAACCCTTGCAG 1935
QY 1945 TTACTGTGTGTGTCTTCTCCCAAGCAAGCACTGTGGTGTGTCCAGAGCTTCTGCCCCA 2004
DB 1936 TTACTGTGTGTGTCTTCTCCCAAGCAAGCACTGTGGTGTGTCCAGAGCTTCTGCCCCA 1995
QY 2005 GCAGTTTGTGCTTGTGACGTCACACCTGCAACCCCTGCAACACTGTGCAACCGTTC 2064
DB 1996 GCAGTTTGTGCTTGTGACGTCACACCTGCAACCCCTGCAACACTGTGCAACCGTTC 2055
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DB 2056 CTCTCCCGGAGCAAGCCGAGCACTGCTTGTGCTGTGTCTTGTCTTGTGATTAAGCTTC 2115
QY 2125 AAGCCTGGCCCTTGTACCCCTCTTCCACCAACTCTCTGTGCCCCCAAGGTCAAGGG 2184
DB 2116 AAGCCTGGCCCTTGTACCCCTCTTCCACCAACTCTCTGTGCCCCCAAGGTCAAGGG 2175
QY 2185 GCCCTAGGAACCTCGAAGCTGTCTCTGCTTTCATCTGTGGGTGTTCAGAAAGATGA 2244
DB 2176 GCCCTAGGAACCTCGAAGCTGTCTCTGCTTTCATCTGTGGGTGTTCAGAAAGATGA 2235
QY 2245 AGAAGAAAATGATGTCTGTGAATGTGTCGTGGAGTGTTAATCAAGAGAACAAAT 2304
DB 2236 AGAAGAAAATGATGTCTGTGAATGTGTCGTGGAGTGTTAATCAAGAGAACAAAT 2295
QY 2305 TGTCTGAGAGCTCAGGGCTGTGATTTGGCAGGTGTGGCTCCACGCTTCTCCCTCCGCT 2364
DB 2296 TGTCTGAGAGCTCAGGGCTGTGATTTGGCAGGTGTGGCTCCACGCTTCTCCCTCCGCT 2355
QY 2365 AAGGCTTCGAGCTGTGCACTGTGCTTGTGCCCCAGCCGCTTGGGCTCACACA 2424
DB 2356 AAGGCTTCGAGCTGTGCACTGTGCTTGTGCCCCAGCCGCTTGGGCTCACACA 2415
QY 2425 GGCCTGTGTGAGCAAGCTGTGCCCCGAGCACTGTGTTGTCTACCCAGAGACTTGTGGGGT 2484
DB 2416 GGCCTGTGTGAGCAAGCTGTGCCCCGAGCACTGTGTTGTCTACCCAGAGACTTGTGGGGT 2475
QY 2485 GTTGGAGAGAGGGGCTCCGGCTGGGCTCCGAGGCTCCCAAGGCTGCAAGGGGCGGTCCAGA 2544
DB 2476 GTTGGAGAGAGGGGCTCCGGCTGGGCTCCGAGGCTCCCAAGGCTGCAAGGGGCGGTCCAGA 2535
QY 2545 GGAAGTGTCCGGGAGAGGGGCTTCCGCAATGTGTGTGCAACCCGTCACAGCGCTCTGC 2604
DB 2536 GGAAGTGTCCGGGAGAGGGGCTTCCGCAATGTGTGTGCAACCCGTCACAGCGCTCTGC 2595
QY 2605 ATGCTCTCTGTGCTGTGCGCTGCGCTGTGCGCTGCAACCGTGAAGTCAATTAAGTGT 2664
DB 2596 ATGCTCTCTGTGCTGTGCGCTGCGCTGTGCGCTGCAACCGTGAAGTCAATTAAGTGT 2655
QY 2665 ATTTTGTAAAAAATTTTAAAAA 2688
DB 2656 ATTTTGTAAAAAATTTTAAAAA 2679

RESULT 10
AAK59167
ID AAK59167 standard; cDNA; 2689 BP.
XX AAK59167;
AC AAK59167;
XX
DT 06-SEP-1999 (first entry)
XX Human G protein coupled receptor flh445 cDNA.
DE

XX G protein coupled receptor; flh8495; human; diagnosis; screening;
KW therapy; antiparkinsonian; nootropic; neuroprotective; neuroplastic;
KW antidepressant; antiarrhythmic; antidiabetic; antiinflammatory;
KW phosphatidylinositol; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 291..1628
FT /tag= a
FT /note= "this region is specifically claimed in claim 7a"
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PD WO928470-A1.
XX
XX 10-JUN-1999.
XX
XX 04-DEC-1998; 98WO-US025832.
XX
XX 04-DEC-1997; 97US-00985090.
XX 17-MAR-1998; 98US-00042780.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Goodenarl ADJ, Gluckmann MA, Xie M, Dietefano P;
XX WPI; 1999-394858/33.
XX P-PsDB; AA106322.
XX
XX New nucleic acid encoding an isolated G-protein coupled receptor useful
XX for treating nervous system related disorders.
XX
XX Claim 7a; Fig 1; 140pp; English.
XX
XX This nucleotide sequence, the coding region of which is claimed, codes
XX for a novel human G protein coupled receptor, termed flh8495 (see
XX AA106322). The flh8495 cDNA was identified in a human cerebellum cDNA
XX library using a rat flh8495 fragment (see also AAX59168) as probe. The
XX invention provides human, rat and mouse flh8495 polynucleotides
XX (including polynucleotides encoding the transmembrane regions of flh8495
XX and antisense nucleic acid molecules), expression vectors, host cells,
XX transgenic animals, flh8495 polypeptides and antibodies, and a method of
XX modulating phosphatidylinositol metabolism. The flh8495 polypeptides can
XX (i) interact with a flh8495 ligand, such as acetylcholine or carnitine,
XX (ii) interact with a G protein or another protein which naturally binds
XX to flh8495, (iii) modulate the activity of an ion channel (e.g. a calcium
XX activated chloride channel or a potassium or calcium channel), (iv)
XX modulate cytosolic ion, e.g. calcium concentration, (v) modulate the
XX release of a neurotransmitter, e.g. acetylcholine or carnitine from a
XX neuron, (vi) modulate a flh8495 ligand response in a responsive cell,
XX (vii) signal ligand binding via phosphatidylinositol turnover, and (viii)
XX modulate phospholipase C activity. The products can be used to treat:
XX disorders mediated by abnormal flh8495 polypeptide activity such as
XX nervous system related disorders e.g. amnesia, apraxia, agnosia,
XX amnesic dysnomia, amnesic spatial disorientation, Kliver-Bucy syndrome,
XX Alzheimer's related memory loss and learning disability; disorders
XX affecting consciousness such as visual hallucinations, petequeal
XX disturbances or delirium associated with Lewy body dementia, schitzo-
XX effective disorders, schizophrenia with mood swings, depressive illness
XX (primary and secondary); affective disorders such as RSM sleep
XX abnormalities in patients suffering from e.g. depression, paradoxical
XX sleep abnormalities, sleep-wakefulness, and body temperature or
XX respiratory depression abnormalities during sleep; disorders affecting
XX pain generation mechanisms e.g. pain related to irritable bowel syndrome
XX or chest pain; movement disorders e.g. Parkinson's disease related
XX movement disorders; eating disorders e.g. insulin hypersecretion related
XX obesity or drinking disorders, e.g. diabetic polydipsia; smooth muscle
XX related disorders, e.g. irritable bowel syndrome, diverticular disease,
XX urinary incontinence, oesophageal achalasia or chronic obstructive
XX airways disease; cardiac muscle disorders, e.g. pathological bradycardia or
XX tachycardia, arrhythmia, flutter or fibrillation; and gland related
XX disorder such as xerostomia or diabetes mellitus. The products can also
XX be used for detection, diagnosis and drug screening

XX
SQ Sequence 2689 BP; 393 A; 990 C; 806 G; 500 T; 0 U; 0 Other;
Query Match 97.6%; Score 2635.2; DB 2; Length 2689;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
QY
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DB CGCAGCGGAGCGGCTCAGGCTCCGAGCTCTCTCTCCGCTGAGCAGCCGCGGCTGCGGCGC 77
QY 85 CCACTGAGCTCGAGTCCGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 144
DB CCACTGAGCTCGAGTCCGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 137
QY 145 GCCCGCGGAGCAGTCCGAGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 204
DB GCCCGCGGAGCAGTCCGAGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 196
QY 138 GCCCGCGGAGCAGTCCGAGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 254
DB AGACGAGGCTCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 256
QY 197 AGACGAGGCTCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 256
DB CCGCGCTCCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 316
QY 257 CCGCGCTCCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 384
DB GCTGAAAGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 376
QY 317 GCTGAAAGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 444
DB CTTGGAAGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 436
QY 377 CTTGGAAGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 504
DB GCTGGAAGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 496
QY 445 GCTGGAAGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 564
DB GCTGGAAGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 556
QY 497 CAACTTCTTCTGCTCAACCTGCGCATCTTCTGCGGCGGCGGCGGCGGCGGCGGCGGCTT 624
DB ACTGATGATACCTTATGCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 616
QY 557 ACTGATGATACCTTATGCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 684
DB GTGGCTGATGATACCTTATGCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 676
QY 617 GTGGCTGATGATACCTTATGCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 744
DB GTGGCTGATGATACCTTATGCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 736
QY 677 GTGGCTGATGATACCTTATGCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 804
DB GTGGCTGATGATACCTTATGCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 804
QY 745 GTGGCTGATGATACCTTATGCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 796
DB GTGGCTGATGATACCTTATGCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 864
QY 805 AGCATCTGATGATACCTTATGCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 856
DB AGCATCTGATGATACCTTATGCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 856
QY 797 AGCATCTGATGATACCTTATGCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 924
DB TGGCGATGATCTTCAACCTGATCTTCAACCTGATCTTCAACCTGATCTTCAACCTGATCTT 916
QY 857 TGGCGATGATCTTCAACCTGATCTTCAACCTGATCTTCAACCTGATCTTCAACCTGATCTT 964
DB GCGCTTCTCAAGCTTCAACCTGATCTTCAACCTGATCTTCAACCTGATCTTCAACCTGATCTT 976
QY 917 GCGCTTCTCAAGCTTCAACCTGATCTTCAACCTGATCTTCAACCTGATCTTCAACCTGATCTT 1044
DB CCGCTTCTCAAGCTTCAACCTGATCTTCAACCTGATCTTCAACCTGATCTTCAACCTGATCTT


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Db 977 CCGCCTCCGCGTGGATGGGGCTCGAGAGGCGAGCCGAGCCCTCCGAGGAGCCCA 1036
QY 1045 GCCCTCAACCAACCCCAACCGCTTGGCTGTGGGGCTGTGGGCAAGAGGGGCAACGGAGAGC 1104
Db 1037 GCCCTCAACCAACCCCAACCGCTTGGCTGTGGGGCTGTGGGCAAGAGGGGCAACGGAGAGC 1096
QY 1105 CATGCCGCTGCAACAGGTATGGGGTGGGTGAGGCGGCGTGAAGCGCTGAGGCCGGGAGAGC 1164
Db 1097 CATGCCGCTGCAACAGGTATGGGGTGGGTGAGGCGGCGTGAAGCGCTGAGGCCGGGAGAGC 1156
QY 1165 GACCCCTCGGGGGGTGGGGGTGGGGCGGCTCCGTGGCTTCAACCCACTCCAGCTCCGGCAG 1224
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QY 1225 CTCCTCGAGGGGCACTGAGAGGGCGGCGCTCACTCAAGAGGGGCTCCAGCGCGTGGCGTTC 1284
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QY 1285 CTCGGGCTTCGCTGAGAGAGCGCATGGAAGTGTGTCCAGAGCTTTCAGCCAGCGCTTTTG 1344
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Db 1397 CTGTGTGGGCCCCATACAGCTGTGTGATGATCATCCGGGCGCGCTGCGCATGAGCACTGCGT 1456
QY 1465 CCCTGACTACTGTGATGAGAACTCTCTTCTGTGGGCTCTGTGGGCAACTCGGCTGTCAACC 1524
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QY 1585 CCAGAGGCTCAAAATTCAGACCCCAACAGCTCCCTGAGAGCATGTGTGAGAGTGAATGAGCCCA 1644
Db 1577 CCAGAGGCTCAAAATTCAGACCCCAACAGCTCCCTGAGAGCATGTGTGAGAGTGAATGAGCCCA 1636
QY 1645 CCAGAGGCTCCCTCAGCCACGCGCTCTCTGAGCCAGAGTCTCTGTGGGCACTGTGGCCCTGCT 1704
Db 1637 CCAGAGGCTCCCTCAGCCACGCGCTCTCTGAGCCAGAGTCTCTGTGGGCACTGTGGCCCTGCT 1696
QY 1705 GCGCCCTACCGGCTCGTTCCTCCAGGGGTGAGCCCGCGGTGTCTGTGGGCTCTCTTCA 1764
Db 1697 GCGCCCTACCGGCTCGTTCCTCCAGGGGTGAGCCCGCGGTGTCTGTGGGCTCTCTTCA 1756
QY 1765 ATGCCAGGCAAGCAACCTGCGCATGAGAGCGCTTCTGTGGGTGGCCAGAGGGCCCTCTCA 1824
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Db 1817 CTGGCTGAGCTGAGAGGCTGGGGTGGCGGCTTGGCCCAATTCTGAGCTCAACCGGAG 1875
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Db 1876 GGGACAGTGTGAGAGTCCCAAGACATGCTGCCACCCCTGTGTGGTCCCACTTGTGAG 1935
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Db 1936 TTAAGTGTGTGTGTCTTCCAAAGAGAGCACTGTGGGTGTGCTCAGAGGCTCTGTGAGCTCA 1995
QY 2005 GAGATTGTGCTGTGACAGTGCACACCTGTGACACCCCTGTGACACACCTGTGACACCGTTC 2064
Db 1996 GAGATTGTGCTGTGACAGTGCACACCTGTGACACCCCTGTGACACACCTGTGACACCGTTC 2055
QY 2065 CTCTCCCGGAGACAGCCCAAGACACTGTCTTGTGCTGTCTGTGCTTAAGCTTC 2124
Db 2056 CTCTCCCGGAGACAGCCCAAGACACTGTCTTGTGCTGTCTGTGCTTAAGCTTC 2115
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QY 2125 AGGCGTGGCCCTTTCACCCCTTCTCCACCACTCTCTGCCCCCAAAAGTGCAGAGG 2184
Db 2116 AGGCGTGGCCCTTTCACCCCTTCTCCACCACTCTCTGCCCCCAAAAGTGCAGAGG 2175
QY 2185 GCCCTAGAACTCGAAGCTGTCTCTGCTTTCCATTCTGGGTGTTTCAAGAGATGA 2244
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QY 2245 AGAAGAAACATGTCTGTAATGTTGCGGGAGTGTAAATCAAGAGACAAAAAT 2304
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QY 2365 AAGGCTTCGGGCTGAGCTGTGCAAGCTGTTCTGCCCACCCGCTCTGGGCTCACACA 2424
Db 2356 AAGGCTTCGGGCTGAGCTGTGCAAGCTGTTCTGCCCACCCGCTCTGGGCTCACACA 2415
QY 2425 GCGCTGTGGCCAGCGTGGCCCGGCACTGTTTGTCTACCCAGAACCTGTGGGGGTT 2484
Db 2416 GCGCTGTGGCCAGCGTGGCCCGGCACTGTTTGTCTACCCAGAACCTGTGGGGGTT 2475
QY 2485 GTTGGAGAGAGGGGCGCGGCTGGGCGCGAGGGTCCAAAGCGTGCAGGGGCGGTTCAGA 2544
Db 2476 GTTGGAGAGAGGGGCGCGGCTGGGCGCGAGGGTCCAAAGCGTGCAGGGGCGGTTCAGA 2535
QY 2545 GGAAGTCCCCGGGCAAGGGGCGCTTGCATGTGTCTGTGACACCGCTGCAACCGCTTGC 2604
Db 2536 GGAAGTCCCCGGGCAAGGGGCGCTTGCATGTGTCTGTGACACCGCTGCAACCGCTTGC 2595
QY 2605 ATGCTCTCTGCTGTGCGCGGCTGCGCTGCGCTGCAACCGTGAAGTCAATAAAGTGT 2664
Db 2596 ATGCTCTCTGCTGTGCGCGGCTGCGCTGCGCTGCAACCGTGAAGTCAATAAAGTGT 2655
QY 2665 ATTTTAAAAA 2688
Db 2656 ATTTTAAAAA 2679

RESULT 11
AAH44572
ID AAH44572 standard; cDNA; 2689 BP.
XX
AC AAH44572;
XX
DT 20-MAR-2003 (revised)
XX
DT 01-NOV-2001 (first entry)
XX
DE Human muscarinic acetylcholine receptor 6 encoding cDNA SEQ ID NO:1.
XX
XX Human; muscarinic acetylcholine receptor 6; mAChR-6; detection;
XX antiparkinsonian; nootropic; neuroprotective; neuroleptic; antidiabetic;
XX antidepressant; antirhythmic; antiinflammatory; cartiline; pain;
XX G-protein coupled receptor; nervous system related disorder; xerostomia;
XX disorders affecting consciousness; affective disorder; movement disorder;
XX irritable bowel syndrome; drinking disorder; gland related disorder;
XX smooth muscle related disorder; cardiac muscle disorder; eating disorder;
XX diabetes mellitus; diagnosis; drug screening; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 291..1628
FT FT /*tag= a
FT PN /product= "muscarinic acetylcholine receptor 6"
XX
XX US6093545-A.
XX
XX 25-JUL-2000.
XX
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1637	Db		CCAGAGGCTCCCTCAGCACAGCCCTCTCTCAGCCACAGGTCTCCTGGGCATCTGGGCCCTGCT	1696
1705	Qy		GCCCCCTACCCGGCTCGTTCCCCAGGGGTGAGCCCGCCGCTGTCTGTGSCCTCTCTTA	1764
1697	Db		GCCCCCTACCCGGCTCGTTCCCCAGGGGTGAGCCCGCCGCTGTCTGTGSCCTCTCTTA	1756
1765	Qy		ATGCCAGGCAGCCACCTGCATGAGAGGCGCTTCTTGGGTGGCCAGAGGGCCCTCA	1824
1757	Db		ATGCCAGGCAGCCACCTGCATGAGAGGCGCTTCTTGGGTGGCCAGAGGGCCCTCA	1816
1825	Qy		CTGCTCGACTGGAGGTGGGTGGCCGGCCCTGCCCCCACTTCTGGCTCCACCGGGA	1884
1817	Db		CTGCTCGACTGGAGGTGGGTGGCCGGCCCTGCCCCCACTTCTGGCTCCACCGGGA	1875
1885	Qy		GGACAGCTCGAGGTCCACAGCATGTGCCACACCCCTGCTGGTGCCACCCCTTCGCAG	1944
1876	Db		GGACAGCTCGAGGTCCACAGCATGTGCCACACCCCTGCTGGTGCCACCCCTTCGCAG	1935
1945	Qy		TTACTGTTGGTGTCTTCCAAAGACGACCTGGGTGTCTCAGGCTTCCTGCCCCCTA	2004
1936	Db		TTACTGTTGGTGTCTTCCAAAGACGACCTGGGTGTCTCAGGCTTCCTGCCCCCTA	1995
2005	Qy		GCAGTTTGCCTCTGCACGTGCACACCTGCACACCCCTGCACACCTGCACACCGTCC	2064
1996	Db		GCAGTTTGCCTCTGCACGTGCACACCTGCACACCCCTGCACACCTGCACACCGTCC	2055
2065	Qy		CTCTCCCGGACAGCCAGGACACTGCCCTTGTGCTTCTGTCTCTGTGATAAGGCTC	2124
2056	Db		CTCTCCCGGACAGCCAGGACACTGCCCTTGTGCTTCTGTCTCTGTGATAAGGCTC	2115
2125	Qy		AGGCTCGGCCCTTTCAACCCCTCTTCCCAACAACTCTCTGCCCCCAAAAGTGTCAAGG	2184
2116	Db		AGGCTCGGCCCTTTCAACCCCTCTTCCCAACAACTCTCTGCCCCCAAAAGTGTCAAGG	2175
2185	Qy		GCCTTAGAACCTCGAGAGCTTCTCTGCTTTTCCATCTGGGTGTTTTCAGAAAGATGA	2244
2176	Db		GCCTTAGAACCTCGAGAGCTTCTCTGCTTTTCCATCTGGGTGTTTTCAGAAAGATGA	2235
2245	Qy		AGAAGAAAACATGTCTGAACTTGATGTTCTGGGATGTTTAAATCAAGAGAGACAAAT	2304
2236	Db		AGAAGAAAACATGTCTGAACTTGAATGTTCTGGGATGTTTAAATCAAGAGAGACAAAT	2295
2305	Qy		TGCTGAGGAGCTCAGGCTCGAATGGCAGGTGGGTCCACGCCCTCTCCTCCGCT	2364
2296	Db		TGCTGAGGAGCTCAGGCTCGAATGGCAGGTGGGTCCACGCCCTCTCCTCCGCT	2355
2365	Qy		AAGCTTCCGGCTGAGCTGTGCCAGCTCTTCTGCCACACCCCGCTCTGGGCTCACACCA	2424
2356	Db		AAGCTTCCGGCTGAGCTGTGCCAGCTCTTCTGCCACACCCCGCTCTGGGCTCACACCA	2415
2425	Qy		GCCCTGTGGCAGAGCTGCCCGCGCCACTCTGTTTCTCACCCAGACCTCTGGGGGTT	2484
2416	Db		GCCCTGTGGCAGAGCTGCCCGCGCCACTCTGTTTCTCACCCAGACCTCTGGGGGTT	2475
2485	Qy		GTTGGGAGGAGGGGCCCGGTGGGCCCGAGGGTCCCAAGCGGTGCAGGGGCGGTCCAGA	2544
2476	Db		GTTGGGAGGAGGGGCCCGGTGGGCCCGAGGGTCCCAAGCGGTGCAGGGGCGGTCCAGA	2535
2545	Qy		GGAGGTGCCCGGGCAGGGGCGCTTCGCCCATGTGCTGTGACCCGCTGCCACGGGCTCTGC	2604
2536	Db		GGAGGTGCCCGGGCAGGGGCGCTTCGCCCATGTGCTGTGACCCGCTGCCACGGGCTCTGC	2595
2605	Qy		ATGCTCTCTGTGCTGCCGCTGCCCTGCAACCGTGAAGGTCACAATAAGTGT	2664
2596	Db		ATGCTCTCTGTGCTGCCGCTGCCCTGCAACCGTGAAGGTCACAATAAGTGT	2655
2665	Qy		ATTTTTTTAAAAAAAAAAAAAAAAAA	2688

DB	2656	ATTTTAAAAA	2679
RESULT	12		
ABX11852			
ID	ABX11852	standard; cDNA; 2689 BP.	
AC	ABX11852;		
XX			
DT	10-MAY-2003	(first entry)	
XX			
DE	Human cDNA encoding muscarinic acetylcholine receptor 6, mAChR-6.		
XX			
KW	Human; ss; gene; mAChR-6; muscarinic acetylcholine receptor-6;		
KW	cognitive disorder; amnesia; amnesic spatial disorientation;		
KW	Klüver-Bucy syndrome; Alzheimer's related memory loss;		
KW	learning disability; consciousness disorder; visual hallucination;		
KW	delirium; schizo-effective disorder; schizophrenia; depression;		
KW	affective disorder; sleep disorders; pain generation disorder;		
KW	irritable bowel syndrome; chest pain; movement disorder;		
KW	Parkinson's disease; eating disorder; insulin hypersecretion obesity;		
KW	heart muscle disorder; bradycardia; tachycardia; arrhythmia; flutter;		
KW	fibrillation; gland related disorder; xerostomia; diabetes mellitus.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	291..1628	
FT		/*tag= a	
FT		/product= "mAChR-6"	
XX			
PN	US2002166131-A1.		
XX			
PD	07-NOV-2002.		
XX			
PF	08-JUL-1999;	99US-00349755.	
XX			
PR	04-DEC-1997;	97US-00985090.	
PR	17-MAR-1998;	98US-00042780.	
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Goodearl ADJ, Gluckemann MA;		
PI			
DR	WPI: 2003-298709/29.		
DR	P-PSDB; ABG76405.		
XX			
PT	New muscarinic acetylcholine receptor 6 (mAChR-6) nucleic acids and		
PT	proteins, useful for modulating acetylcholine or phosphatidylinositol,		
PT	particularly for treating e.g. schizophrenia, chest pain, tachycardia or		
PT	arrhythmia.		
XX			
PS	Claim 7; Fig 1; 66pp; English.		
XX			
CC	The invention relates to an isolated human or rat muscarinic		
CC	acetylcholine receptor 6 (mAChR-6) nucleic acid molecule and the encoded		
CC	protein. Also included are (non-human) host cells comprising the mAChR-6		
CC	nucleic acid molecule, an antibody that selectively bind the polypeptide		
CC	above, a method for producing the polypeptide by culturing the host cell		
CC	such that the mAChR-6 nucleic acid is expressed, a method for detecting		
CC	the presence of the mAChR-6 polypeptide and nucleic acid, a method for		
CC	identifying a compound that binds to the mAChR-6 polypeptide and a method		
CC	for modulating the activity of the mAChR-6 polypeptide. The mAChR-6		
CC	polynucleotide, polypeptide, antibody or modulator are useful in drug		
CC	screening assays, diagnostic assays for identifying diseases, allelic		
CC	screening, pharmacogenetic testing, methods of treatment,		
CC	pharmacogenomics or monitoring the effects during clinical trials. In		
CC	particular, the mAChR-6 polynucleotide, polypeptide or antibody is useful		
CC	for treating or diagnosing cognitive disorders (e.g. amnesia, amnesic		
CC	spatial disorientation, Klüver-Bucy syndrome, Alzheimer's related memory		
CC	loss or learning disability), disorders affecting consciousness (e.g.		
CC	visual hallucinations or delirium), schizo-effective disorders (e.g.		
CC	schizophrenia or depression), affective disorders (e.g. sleep disorders)		

QY	481	CGACTCGAGCCTCCGCAACCCAGAACTTCTTCTGCTCAACCTCGCCATCTCCGACTT	540
Db	481	CGACTCGAGCCTCCGCAACCCAGAACTTCTTCTGCTCAACCTCGCCATCTCCGACTT	540
QY	541	CCTCGTCCGGCGCTTCTGCACTCCACTGATATGTAACCTACGTCGTCGACAGCGCGCTGGAC	600
Db	541	CCTCGTCCGGCGCTTCTGCACTCCACTGATATGTAACCTACGTCGTCGACAGCGCGCTGGAC	600
QY	601	CTTTCGGCCGGGCTCTGCAAGCTGTGGCTGTGTAGTGGACTACCTGCTGTGACACTCCCTC	660
Db	601	CTTTCGGCCGGGCTCTGCAAGCTGTGGCTGTGTAGTGGACTACCTGCTGTGACACTCCCTC	660
QY	661	TGCTTCAAATCGTGTCTCATCAGCTACGACCGCTTCTGTCCGTCACCCGAGCGGTCTC	720
Db	661	TGCTTCAAATCGTGTCTCATCAGCTACGACCGCTTCTGTCCGTCACCCGAGCGGTCTC	720
QY	721	ATACCGGGCCGACAGGGGTGACACCGGGGGGCGAGTCGGGAAGATGCTGCTGTGGGT	780
Db	721	ATACCGGGCCGACAGGGGTGACACCGGGGGGCGAGTCGGGAAGATGCTGCTGTGGGT	780
QY	781	GCTGCGCTTCTGCTGTACGGACACGACCATCTGAGCTGGGAGTACCTGTCCGGGGGAG	840
Db	781	GCTGCGCTTCTGCTGTACGGACACGACCATCTGAGCTGGGAGTACCTGTCCGGGGGAG	840
QY	841	CTCCATCCCGAGGGCCACTGCTATGCCGAGTTCCTTCTACAACTGCTCTTCTCATCAC	900
Db	841	CTCCATCCCGAGGGCCACTGCTATGCCGAGTTCCTTCTACAACTGCTCTTCTCATCAC	900
QY	901	GGCTTCCACCTCGAGTTCCTTACCGCTTCTCAGCGTCACTTCCTTAACTCAGCAT	960
Db	901	GGCTTCCACCTCGAGTTCCTTACCGCTTCTCAGCGTCACTTCCTTAACTCAGCAT	960
QY	961	CTACTGAATCCAGAGCGCACCGCTCTCGGCTGGATGGGCTCGAGAGCGACGCGG	1020
Db	961	CTACTGAATCCAGAGCGCACCGCTCTCGGCTGGATGGGCTCGAGAGCGACGCGG	1020
QY	1021	CCCGAGCGCTCCCGAGGGCCAGCCCTCACACCCCGCCCTGGCTGTGGGGGTG	1080
Db	1021	CCCGAGCGCTCCCGAGGGCCAGCCCTCACACCCCGCCCTGGCTGTGGGGGTG	1080
QY	1081	CTGGAGAAAGGGGACGGGGAGGCGATGCGCTGACACAGGTATGGGGTGGGTGAGCGCGC	1140
Db	1081	CTGGAGAAAGGGGACGGGGAGGCGATGCGCTGACACAGGTATGGGGTGGGTGAGCGCGC	1140
QY	1141	CGTAGCGCTGAGCGCGGGGAGGCGACCTCGGGGGTGGCGTGGGGCGGCTCGGTGCG	1200
Db	1141	CGTAGCGCTGAGCGCGGGGAGGCGACCTCGGGGGTGGCGTGGGGCGGCTCGGTGCG	1200
QY	1201	TTTACCCCACTCCAGCTCCGGCAGCTCTCGAGGGGCACTGAGAGGCGCGCTCACTCAA	1260
Db	1201	TTTACCCCACTCCAGCTCCGGCAGCTCTCGAGGGGCACTGAGAGGCGCGCTCACTCAA	1260
QY	1261	GAGGGCTCCAAAGCGGTGCGCTCTCGGCTGCTGGAGAAAGCGCATGAAGTGGTGTG	1320
Db	1261	GAGGGCTCCAAAGCGGTGCGCTCTCGGCTGCTGGAGAAAGCGCATGAAGTGGTGTG	1320
QY	1321	CGAGAGCTTACCCAGCGCTTTCGGCTGTCTC- GGGACAGGAAGTGGCCAAAGTGGCTGG	1379
Db	1321	CGAGAGCTTACCCAGCGCTTTCGGCTGTCTC- GGGACAGGAAGTGGCCAAAGTGGCTGG	1380
QY	1380	CGGTCACTCGTAGCATCTTTTGGGCTCTGCTGGGCGCCATACACGCTGCTGATGATCATCC	1439
Db	1381	CGGTCACTCGTAGCATCTTTTGGGCTCTGCTGGGCGCCATACACGCTGCTGATGATCATCC	1440
QY	1440	GCGCGCTGCGCATGGCCACTGCGTCCCTGACTACTGTGATCGAAACCTCTTCTGGCTCC	1499
Db	1441	GCGCGCTGCGCATGGCCACTGCGTCCCTGACTACTGTGATCGAAACCTCTTCTGGCTCC	1500
QY	1500	TGTGGGCCAACTCGCGCTGTCAACCTCTCTTACCTCTGTGCCACCACTCTCCGCG	1559
Db	1501	TGTGGGCCAACTCGCGCTGTCAACCTCTCTTACCTCTGTGCCACCACTCTCCGCG	1560

RESULT 14
AAS62391
ID AAS62391 standard; cDNA; 2173 BP.
XX

QY	1560	GGGCTTCAACCAAGCTGTCTGCCCCCAGAAAGCTCAAAATCCAGCCCCACAGCTCCCTGG	1619
Db	1561	GGGCTTCAACCAAGCTGTCTGCCCCCAGAAAGCTCAAAATCCAGCCCCACAGCTCCCTGG	1620
QY	1620	AGCACTGCTGGAAGTGAAGTGGCCACCAAGAGCTCCCTCAGCCACAGCTCTCTCAGCCCA	1679
Db	1621	AGCACTGCTGGAAGTGAAGTGGCCACCAAGAGCTCCCTCAGCCACAGCTCTCTCAGCCCA	1680
QY	1680	GGTCTCTCTGGGCACTTGGGCCCTGCTGCCCTTACCCGGCTCGTTCCCCAGAGGGGTGAGCC	1739
Db	1681	GGTCTCTCTGGGCACTTGGGCCCTGCTGCCCTTACCCGGCTCGTTCCCCAGAGGGGTGAGCC	1740
QY	1740	CGCGCGTGTCTGTGGCCCTCTCTTAATGCCACGGGAGCCACCCCTGTCATGAGAGGGCGCTT	1799
Db	1741	CGCGCGTGTCTGTGGCCCTCTCTTAATGCCACGGGAGCCACCCCTGTCATGAGAGGGCGCTT	1800
QY	1800	CCTGGGTTGGCCAGAGGGCCCTCACTGGCTGGACTGGAGGCTGGGTGGCGGCCCTGCCC	1859
Db	1801	CCTGGGTTGGCCAGAGGGCCCTCACTGGCTGGACTGGAGGCTGGGTGGCGGCCCTGCCC	1860
QY	1860	CCCCACATTTCTGGCTCCACCGGGAGGGACAGTCTGGAGGTCCTAGACATGCTGCCACAC	1919
Db	1861	CCCCACATTTCTGGCTCCACCGGGAGGGACAGTCTGGAGGTCCTAGACATGCTGCCACAC	1920
QY	1920	CCCTGCTGTGTCGCCACCCCTTCGACGTTACTGTTGGTGTCTTCCCAAAGCAAGACCTG	1979
Db	1921	CCCTGCTGTGTCGCCACCCCTTCGACGTTACTGTTGGTGTCTTCCCAAAGCAAGACCTG	1980
QY	1980	GGTGTGCTCCAGGCTTCTGCCCTAGCAGTTGCTGCTGACAGTGCACAGTGCACACCTGCACAC	2039
Db	1981	GGTGTGCTCCAGGCTTCTGCCCTAGCAGTTGCTGCTGACAGTGCACAGTGCACACCTGCACAC	2040
QY	2040	CCCTGCACACACTGCACACCGCTCCTCTCCCGGAGCAAGCCAGGACACTGCTTTTGCT	2099
Db	2041	CCCTGCACACACTGCACACCGCTCCTCTCCCGGAGCAAGCCAGGACACTGCTTTTGCT	2100
QY	2100	GCCTTCTGTCTTGCATAAAGCTCAGGCTGGCCCTTTTACCCCTCTTCCCAACCAATC	2159
Db	2101	GCCTTCTGTCTTGCATAAAGCTCAGGCTGGCCCTTTTACCCCTCTTCCCAACCAATC	2160
QY	2160	TCTCTGCCCGCCAAAGTGTCAAGGGGCCCTAGGAACCTCGAAGCTGTTCTTGTCTTTTCC	2219
Db	2161	TCTCTGCCCGCCAAAGTGTCAAGGGGCCCTAGGAACCTCGAAGCTGTTCTTGTCTTTTCC	2220
QY	2220	ATTCTGGGTGTTTTTCAGAAAGATGAAGAGAAAATCATGTCTGTGAATTTGATGTTCTGTG	2279
Db	2221	ATTCTGGGTGTTTTTCAGAAAGATGAAGAGAAAATCATGTCTGTGAATTTGATGTTCTGTG	2280
QY	2280	GATGTTTAAATCAAGAGAGACAAAATTTGCTGAGGAGCTCAGGGCTGGATTTGGCAGGTTGG	2339
Db	2281	GATGTTTAAATCAAGAGAGACAAAATTTGCTGAGGAGCTCAGGGCTGGATTTGGCAGGTTGG	2340
QY	2340	GCTCCCAAGCCCTCTCTCCCTCAGGCTTCCGGCTGAGCTGTCAGCTGTCAGCTGCTTCTGC	2399
Db	2341	GCTCCCAAGCCCTCTCTCCCTCAGGCTTCCGGCTGAGCTGTCAGCTGTCAGCTGCTTCTGC	2400
QY	2400	CCACCCCGCTCTGGGCTCACACAGCCCTGTGTGCAAGCCCTGCCCGCCCACTCTGTT	2459
Db	2401	CCACCCCGCTCTGGGCTCACACAGCCCTGTGTGCAAGCCCTGCCCGCCCACTCTGTT	2460
QY	2460	TGCTCACCCAGGACCTCTGGGGTTGTTGGGAGGAGGGGGCCCGGCTGGCGCCGAGGGTC	2519
Db	2461	TGCTCACCCAGGACCTCTGGGGTTGTTGGGAGGAGGGGGCCCGGCTGGCGCCGAGGGTC	2520
QY	2520	CCAAGGCTGCAAGGGCGGTCCAGAGAGGTGCCCGGGGAGGGGGCGCTTCCGCAT	2575
Db	2521	CCAAGGCTGCAAGGGCGGTCCAGAGAGGTGCCCGGGGAGGGGGCGCTTCCGCAT	2576

AC	AAS62391;									
XX	14-FEB-2002 (first entry)									
DT	cDNA sequence #178 encoding novel human secreted protein.									
XX										
DE	Human secreted protein; hyperproliferative disorder; autoimmune disorder;									
XX	immune deficiency disorder; blood disorder; inflammatory disorder;									
KW	infectious disorder; gene therapy; antimicrobial; hepatotropic;									
KW	immunosuppressive; antirheumatic; ss.									
XX										
OS	Homo sapiens.									
XX	WO200177291-A2.									
PN	18-OCT-2001.									
PD										
XX	29-MAR-2001; 2001WO-US010495.									
XX	06-APR-2000; 2000US-0195604P.									
PR	(GEMY) GENETICS INST INC.									
XX										
PA	Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;									
PI	Gulukota K, Graham JR;									
PI	WPI; 2002-010900/01.									
XX										
DR	New polynucleotides encoding secreted proteins useful for treating e.g.									
XX	asthma, HIV and Crohn's disease.									
XX	Claim 1; Page 168; 391pp; English.									
XX	The present invention relates to the isolation of novel cDNA sequences									
CC	which encode human secreted proteins. The cDNA sequences have been									
CC	derived from a variety of human tissues. The invention also provides a									
CC	method for producing proteins from these polynucleotide sequences. The									
CC	proteins are useful for identifying compounds that modulate their									
CC	activity and production, and the cell is also useful for identifying									
CC	compounds that modulate expression of the polynucleotide sequences									
CC	encoding the secreted proteins. The sequences of the invention are useful									
CC	for treating diseases such as hyperproliferative disorders (e.g. cancer,									
CC	immune deficiency disorders (e.g. severe combined immunodeficiency									
CC	(SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders									
CC	(e.g. thrombocytopenia), inflammatory disorders (e.g. arthritis) and									
CC	infectious disorders (e.g. hepatitis). The polynucleotide sequences of									
CC	the invention are also useful in gene therapy. AAS62214-AAS62838									
CC	represent the cDNA sequences of the invention that encode for novel human									
CC	secreted proteins									
XX										
SQ	Sequence 2173 BP; 330 A; 772 C; 620 G; 451 T; 0 U; 0 Other;									
Query Match 79.6%; Score 2149.2; DB 6; Length 2173;										
Best Local Similarity 99.8%; Pred. No. 0;										
Matches 2162; Conservative 0; Mismatches 3; Indels 1; Gaps 1										
QY	508	CTTCTTCTGCTCAACCTCGCATCTCCGACTTCTCTGTCGCGGCTTCTGATCCCCT	567							
Db	1	CTTCTTCTGCTCAACCTCGCATCTCCGACTTCTCTGTCGCGGCTTCTGATCCCCT	60							
QY	568	GTATGTACCTACGTGCTGACAGCGCGTGGACCTTCGGCCGGGGCTCTGCAAGCTGTG	627							
Db	61	GTATGTACCTACGTGCTGACAGGCGGTGGACCTTCGGCCGGGGCTCTGCAAGCTGTG	120							
QY	628	GCTGTTAGTGACTACCTGCTGTGTGCACCTCTCTGCTTCAACATCTGTCATAGCTTA	687							
Db	121	GCTGTTAGTGACTACCTGCTGTGTGCACCTCTCTGCTTCAACATCTGTCATAGCTTA	180							
QY	688	CGACGGCTTCTGTTCGGTCAACCGAGCGTCTCATACGGGGCCACGAGGTCACACGG	747							
Db	181	CGACGGCTTCTGTTCGGTCAACCGAGCGTCTCATACGGGGCCACGAGGTCACACGG	240							
QY	748	CGGGGACGTGGGGAAGATGCTGCTGGTGTGGGTGTGGCTTCTGCTGTACGGACCAG	807							

Qy	1010	GAGCAGCCGGCCCCGAGCCCTTCCGAGGCCCGAGCCCTCA	CGACCCCAACGCGCTGGC	1069	
Db	481	GAGCAGCCGGCCCCGAGCCCTTCCGAGGCCCGAGCCCTCA	CGACCCCAACGCGCTGGC	540	
Qy	1070	TGCTGGGGCTCTGGCAGNAGGGGCGAGGGAGGCCATGCGCTG	CACAGGTATGGGTG	1129	
Db	541	TGCTGGGGCTCTGGCAGNAGGGGCGAGGGAGGCCATGCGCTG	CACAGGTATGGGTG	586	
Qy	1130	GGTGAGGCGGCGTAGGCGCTGAGGCCGGGGAGGCGACCTC	CGGGGGTGGCGTGGGGC	1189	
Db	587	-----	-----	586	
Qy	1190	GGCTCCGTGGTTCA	CCCACTTCAGCTCGGGCAGCTTCCTCGAGGGGCACTGAGAGGCGG	1249	
Db	587	-----	-----	586	
Qy	1250	CGCTCACTCAAGAGGGGCTCC	AGCCGTGGCGTCTCGGCTCGCTGGAGAGCGCATG	1309	
Db	587	-----	-----	586	
Qy	1310	AAGATGGTGTCC	CAGAGCTTCA	CCAGCGCTTTCGGCTGTCTCGGAGCAGAAAGTGCC	1369
Db	587	-----	-----	600	
Qy	1370	AAGTCGTGGCCGTATCGTGAGCATCTTTGGGGCTCTGCTGGG	CCCCCATACA	CGCTGCTG	1429
Db	601	AAGTCGTGGCCGTATCGTGAGCATCTTTGGGGCTCTGCTGGG	CCCCCATACA	CGCTGCTG	660
Qy	1430	ATGATCATTCGGGGCCGCTGCCATGGGCAC	TGGTCCCTGACTACTGGTACGAAACCTCC	1489	
Db	661	ATGATCATTCGGGGCCGCTGCCATGGGCAC	TGGTCCCTGACTACTGGTACGAAACCTCC	720	
Qy	1490	TTCTGGCTCTGTGGGCAACTCGGCTGTCA	AACTCTCTACCTCTGTGCCCACAC	1549	
Db	721	TTCTGGCTCTGTGGGCAACTCGGCTGTCA	AACTCTCTCTACCTCTGTGCCCACAC	780	
Qy	1550	AGCTTCGCGCGGCTTCA	CGAGCTGCTGTGCCCCCAGAGCTCAAAATCGAGCCCCAC	1609	
Db	781	AGCTTCGCGCGGCTTCA	CGAGCTGCTGTGCCCCCAGAGCTCAAAATCGAGCCCCAC	840	
Qy	1610	AGCTCCCTGGAGCACTGCTGGAAGTAGTGCGCCAC	CAGAGCTCTCCCTCAGCCACCGCTC	1669	
Db	841	AGCTCCCTGGAGCACTGCTGGAAGTAGTGCGCCAC	CAGAGCTCTCCCTCAGCCACCGCTC	900	
Qy	1670	TCTCAGCCCCAGTCTCTGGGCACTGGCCCTGTGCTGCC	CCCCCTACCCGGCTCGTTGCCCA	1729	
Db	901	TCTCAGCCCCAGTCTCTGGGCACTGGCCCTGTGCTGCC	CCCCCTACCCGGCTCGTTGCCCA	960	
Qy	1730	GGGGTAGCCCCCGCTGTCTGGGCCCTCTCTTAATG	CCACGGCAGCCACCTGCGCATG	1789	
Db	961	GGGGTAGCCCCCGCTGTCTGGGCCCTCTCTTAATG	CCACGGCAGCCACCTGCGCATG	1020	
Qy	1790	GAGCGCTTCTCGGTTGGCCAGAGGGCCCTC	CACCTGGCTGGAAGTGGGGTGGG	1849	
Db	1021	GAGCGCTTCTCGGTTGGCCAGAGGGCCCTC	CACCTGGCTGGAAGTGGGGTGGG	1080	
Qy	1850	CGGCCCTGCCCCCACTTCTGGCTTCA	CCGGGAGGGA	CAGTCTGGAGTTC	1909
Db	1081	CGGCCCTGCCCCCACTTCTGGCTTCA	CCGGGAGGGA	CAGTCTGGAGTTC	1139
Qy	1910	GCTGCCACCCCTGCTGGTGCCAC	CCCTTGGAGTTACTGGTGGTGTCTTCCCAAG	1969	
Db	1140	GCTGCCACCCCTGCTGGTGCCAC	CCCTTGGAGTTACTGGTGGTGTCTTCCCAAG	1199	
Qy	1970	CAAGCACTGGGTGTCTCAGGCTTCTG	CCCTTAGCAGTTTGCTCTGCACTGCA	2029	
Db	1200	CAAGCACTGGGTGTCTCAGGCTTCTG	CCCTTAGCAGTTTGCTCTGCACTGCA	1259	
Qy	2030	ACCTGCAACCCCTGCACTGCA	CACTGCA	CCGTCCTCTCCCGGA	2089
Db	1260	ACCTGCAACCCCTGCACTGCA	CACTGCA	CCGTCCTCTCCCGGA	1319

[illegible]

Search completed: June 2, 2005, 06:01:44
Job time : 1454.49 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 05:10:00 ; Search time 8897.2 Seconds
(without alignments)
11546.944 Million cell updates/sec

Title: US-10-727-021-5
Perfect score: 2699
Sequence: 1 ccacgcgtccgcgctgca.....aaaaaaaaaaaaaaaaaaaaa 2699

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_ges1.*
9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	767.6	28.4	813	5	BX089742	BX089742
2	743.6	27.6	946	5	BQ068856	BQ068856 AGENCOURT
3	705.2	26.2	1103	4	BM548665	BM548665 AGENCOURT
4	680.8	25.2	732	7	CF147822	CF147822 AGENCOURT
5	549.6	20.4	890	4	BI731453	BI731453 603354331
6	543	20.1	672	6	CB556920	CB556920 AMGNNUC:U
7	522	19.3	533	6	CB154982	CB154982 K-EST0213
8	516	19.1	716	7	CN423054	CN423054 170004245
9	476.6	17.7	910	2	BE783826	BE783826 601471053
10	455	16.9	466	7	CN335777	CN335777 170004245
11	429.6	15.9	842	7	CO403631	CO403631 AGENCOURT
12	390.8	14.5	547	6	CB611519	CB611519 AMGNNUC:N
13	389.4	14.4	653	6	BY727560	BY727560 BY727560
14	386	14.3	409	2	BF531112	BF531112 602072279
15	371.2	13.8	499	2	BF567596	BF567596 UI-R-B00-
16	369.6	13.7	519	2	AW669811	AW669811 113386 MA
17	358.8	13.3	412	7	H30846	H30846 yo78d12.x1
18	352	13.0	434	6	CB758850	CB758850 AMGNNUC:S
19	340.8	12.6	1046	5	BQ950659	BQ950659 AGENCOURT
20	336.6	12.5	401	7	R87217	R87217 yo45e10.r1
21	278.8	10.3	775	9	CC580463	CC580463 CH240_375
22	264.2	9.8	853	6	CD326085	CD326085 AGENCOURT
23	252.8	9.4	782	7	CO872448	CO872448 BovGen_00
24	249.4	9.2	538	2	AW654493	AW654493 103977 MA

25	240.6	8.9	490	6	CB725716	CB725716 AMGNNUC:U
26	224.2	8.3	643	1	AL848045	AL848045 AL848045
27	214.4	7.9	258	2	AW654609	AW654609 104607 MA
28	212	7.9	484	1	AA859887	AA859887 UI-R-E0-C
29	205.6	7.6	646	6	CB437482	CB437482 684956 MA
30	202.8	7.5	832	7	CK769909	CK769909 958021 MA
31	197.8	7.3	975	9	CNS039RV	AL234232 Tetradon
32	190.8	7.1	600	2	BE647364	BE647364 UI-M-BH1-
33	189.8	7.0	236	2	BE063702	BE063702 QV3-BT029
34	185.8	6.9	240	7	R87218	R87218 yo45e10.s1
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37	183.6	6.8	621	1	AA943666	AA943666 EST199165
38	181	6.7	770	7	CO875612	CO875612 BovGen_03
39	180.8	6.7	281	2	BB592940	BB592940 BB592940
40	179.4	6.6	260	7	H28163	H28163 yo78d12.s1
41	179.2	6.6	733	7	CO875634	CO875634 BovGen_03
42	179.2	6.6	734	7	CO872468	CO872468 BovGen_00
43	176	6.5	744	9	CR021310	CR021310 Forward s
44	174	6.4	1048	4	BM805220	BM805220 AGENCOURT
45	173.6	6.4	1440	9	AY404934	AY404934 Homo sapi

ALIGNMENTS

RESULT 1
BX089742
LOCUS BX089742 813 bp mRNA linear EST 23-JAN-2003
DEFINITION BX089742 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone
IMAGE:180906, mRNA sequence.
ACCESSION BX089742
VERSION BX089742.1 GI:27821886
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 813)
Ebert L., Heil, O., Hennig S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGP998G19334.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGAACACGCTATGAC.

FEATURES

source
1..813
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGP998G19334 ; IMAGE:180906"
/sex="Male"
/dev_stages="55-year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b4HB55Y"
/note="Organ: brain; Vector: p77T3D (Pharmacia) with a
modified polylinker; Site1: Not 1; Site2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAACTCTGAAGTGGAGCGCGCTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

ORIGIN	Query Match	28.4%	Score 767.6	DB 5	Length 813	
	Best Local Similarity	98.5%	Pred. No. 3.3e-143			
	Matches 803	Conservative 0	Mismatches 9	Indels 3	Gaps 3	
Qy	1531	CTACCCCTCTGTGCCACACACAGCTTCCGCGGGGCTTCCACCAAG-CTGCTCTGCCCCCAGA	1589			
Db	1	CTACCCCTCTGTGCCACACACAGCTTCCGCGGGGCTTCCACCAAGTCTGCTCTGCCCCCAGA	60			
Qy	1590	AGCTCAAAATCCAGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTGAGTGGCCACCACAGA	1649			
Db	61	AGCTCAAAATCCAGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTGAGTGGCCACCACAGA	120			
Qy	1650	GCTTCCCTCAGCCACAGGCTCTCTCAGGCCCAAGTTCCTGGGCACTCTGGCCCTGCTGCCCC	1709			
Db	121	GCTTCCCTCAGCCACAGGCTCTCTCAGGCCCAAGTTCCTGGGCACTCTGGCCCTGCTGCCCC	180			
Qy	1710	CTACCCGGCTCGTTTCCCCAGGGGTGAGCCCGCGGTCTGTGTGGCCCTCTCTTAATGCC	1769			
Db	181	CTACCCGGCTCGTTTCCCCAGGGGTGAGCCCGCGGTCTGTGTGGCCCTCTCTTAATGCC	240			
Qy	1770	ACGCGACCCACCTGCCATGGAGGCGCTTCTTGGGTTGGCCAGAGGGCCCCCTCACTGGC	1829			
Db	241	ACGCGACCCACCTGCCATGGAGGCGCTTCTTGGGTTGGCCAGAGGGCCCCCTCACTGGC	300			
Qy	1830	TGGACTGGAGGCTGGGTGGCGGCCCTGCCCCCCACAAATTCGGCTCAACGGGGAGGAC	1889			
Db	301	TGGACTGGAGGCTGGGTGGCGGCCCTGCCCCCCACAAATTCGGCTCAAC-GGGAGGGAC	359			
Qy	1890	AGTCTGGAGGTCCACAGCATGCTGCCACACCCCTGCTGGTGCCACACCTTCGCAAGTTACT	1949			
Db	360	AGTCTGGAGGTCCACAGCATGCTGCCACACCCCTGCTGGTGCCACACCTTCGCAAGTTACT	419			
Qy	1950	GTTTGGTGTCTTCCCAAAGCAAGCACTGGGTGTGTCCAGGCTTCCTGCCCTAGCAGT	2009			
Db	420	GTTTGGTGTCTTCCCAAAGCAAGCACTGGGTGTGTCCAGGCTTCCTGCCCTAGCAGT	479			
Qy	2010	TTGCGCTCTGCACGTGCACACCTGCACACCCCTGCACACACCTGCACACCGTCCCTCTC	2069			
Db	480	TTGCGCTCTGCACGTGCACACCTGCACACCCCTGCACACACCTGCACACCGTCCCTCTC	539			
Qy	2070	CCCGACAAGCCAGGACACTGCGCTTTGTCCTTCTGTCTTTGCAATAAGCCTCAGGCC	2129			
Db	540	CCCGACAAGCCAGGACACTGCGCTTTGTCCTTCTGTCTTTGCAATAAGCCTCAGGCC	599			
Qy	2130	TGGCCCTTTTCAACCCCTTCCCAACCACTCTCTGCCCCCAAAAGTGTCAAGGGGCCCT	2189			
Db	600	TGGCCCTTTTCAACCCCTTCCCAACCACTCTCTGCCCCCAAAAGTGTCAAGGGGCCCT	659			
Qy	2190	AGGAACCTCGAAGCTGTTCTCTGCTTTTCCATTCTGGGTGTGTTTTCAGAAAGATGAAGAAG	2249			
Db	660	AGGAACCTCGAAGCTGTTCTCTGCTTTTCCATTCTGGGTGTGTTTTCAGAAAGATGAAGAAG	719			
Qy	2250	AAAACATGCTGTGAACCTTGATGTTCTGCGGATGTTTAAATCAAGAGAGACAAAATTTGCTG	2309			
Db	720	AAAACATGCTGTGAACCTTGATGTTCTGCGGATGTTTAAATCAAGAGAGACAAAATTTGCTG	779			
Qy	2310	AGGAGCTCAGGGCTGGAAATGGCAGGTGTGGGCTCC	2344			

[illegible]

Db 792 AGTGGCACCCACCTGGGACACACCCCTTGGACACACCTTGACACACCGGTCC 844

RESULT 4

CF147822

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF147822 732 bp mRNA linear EST 25-JUL-2003
AGENCOURT 14740187 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:6971899 5', mRNA sequence.

CF147822

CF147822.1 GI:33244090

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 732)

NIH-MGC <http://mgi.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: GPCR Consortium

cDNA Library Preparation: GPCR Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: IRB102 row: b column: 06

High quality sequence stop: 610.

Location/Qualifiers

1..732

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6971899"

/tissue_type="mixed"

/lab_host="DH10B"

/clone_lib="NIH_MGC_145"

/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:

varies by clone; ORFs were PCR-amplified and cloned into

pCDNA3.1 by the GPCR Consortium. Cloning sites vary by

clone and include the following: 5'-EcoRV-XmiI/XhoI-3',

5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).

For information about which gene each clones represents,

please visit our anonymous ftp site at

ftp://image.llnl.gov/image/rearrayed_plates/IRB1.preSV.dat

a Note: this is a NIH_MGC Library."

Query Match 25.2%; Score 680.8; DB 7; Length 732;

Best Local Similarity 98.2%; Pred. No. 8.2e-126;

Matches 699; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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DB 10 CTTGCCATGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 69

QY 352 CGATCGGCG 411

DB 70 CGAGGCG 129

QY 412 CGCGCTCATGGCGCTCATCGTGGCCACCGTGTGGCCACCGTGTGGCTCGC 471

DB 130 CGCGCTCATGGCGCTCATCGTGGCCACCGTGTGGCCACCGTGTGGCTCGC 189

QY 472 CTTCTGGCGCGACTCGAGCCTCGGACCCAGAACAACTTTCTTCTGTCTCAAC 531

DB 190 CTTCTGGCGCGACTCGAGCCTCGGACCCAGAACAACTTTCTTCTGTCTCAAC 249

QY 532 CTCGACTTCTCGTTCGGCGCCTTCTGCATCCCACTGTATGTATACCTACGTGCTGACAGG 591
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QY 592 CCGCTGAGACCTTTCGGCGCGCGCGCTCTGCAAGCTGTGGCTGTGGAGTACCTACCTGCTG 651
DB 310 CCGCTGAGACCTTTCGGCGCGCGCGCTCTGCAAGCTGTGGCTGTGGAGTACCTACCTGCTG 369
QY 652 CACCTCTCTCGCTTCAACATCGTGTGCATCAGCTACGACCGCTTCTGTGGTACCCG 711
DB 370 CACCTCTCTCGCTTCAACATCGTGTGCATCAGCTACGACCGCTTCTGTGGTACCCG 429
QY 712 AGCGGTCTCATACCGGCGCGCGCGCGCTGACACGGCGCGCGCGCTGCGGAAGATGCTGCT 771
DB 430 AGCGGTCTCATACCGGCGCGCGCGCGCTGACACGGCGCGCGCGCTGCGGAAGATGCTGCT 489
QY 772 GGTGTGGTGTGGCTTCTTCTGTGTACGGACAGCCATCTCTGAGCTGGAGTACCTGCTC 831
DB 490 GGTGTGGTGTGGCTTCTTCTGTGTACGGACAGCCATCTCTGAGCTGGAGTACCTGCTC 549
QY 832 CGGGGCGAGCTCCATTCGCCGAGGCGCACTGTATGCCAGTTCCTTCTCAAACTGGTACTT 891
DB 550 CGGGGCGAGCTCCATTCGCCGAGGCGCACTGTATGCCAGTTCCTTCTCAAACTGGTACTT 609
QY 892 CCTCATCAGCGCTTCCACCTTGGAGTTCCTTACGCCCTTCTCTCAGCGTACCTTCTTAA 951
DB 610 CTTTCATCAGCGCTTCCACCTTGGAGTTCCTTACGCCCTTCTCTCAGCGTACCTTCTTAA 669
QY 952 CTTTCATCAGCGCTTCCACCTTGGAGTTCCTTACGCCCTTCTCTCAGCGTACCTTCTTAA 1003
DB 670 CTTTCATCAGCGCTTCCACCTTGGAGTTCCTTACGCCCTTCTCTCAGCGTACCTTCTTAA 720

FEATURES

source

BI731453 890 bp mRNA linear EST 20-SEP-2001
LOCUS 603354331P1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5361966 5',
DEFINITION mRNA sequence.

ACCESSION BI731453

VERSION BI731453.1 GI:15708466

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 890)

NIH-MGC <http://mgi.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11920 row: m column: 07

High quality sequence stop: 811.

Location/Qualifiers

1..890

/organism="Mus musculus"

/mol_type="mRNA"

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/clone="IMAGE:5361966"

/tissue_type="retina"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_94"

/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 3.3 kb. Library enriched for

ORIGIN

Query Match 25.2%; Score 680.8; DB 7; Length 732;
Best Local Similarity 98.2%; Pred. No. 8.2e-126;
Matches 699; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
QY 292 CGGGGCGCATGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 351
DB 10 CTTGCCATGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 69
QY 352 CGATCGGCG 411
DB 70 CGAGGCG 129
QY 412 CGCGCTCATGGCGCTCATCGTGGCCACCGTGTGGCCACCGTGTGGCTCGC 471
DB 130 CGCGCTCATGGCGCTCATCGTGGCCACCGTGTGGCCACCGTGTGGCTCGC 189
QY 472 CTTCTGGCGCGACTCGAGCCTCGGACCCAGAACAACTTTCTTCTGTCTCAAC 531
DB 190 CTTCTGGCGCGACTCGAGCCTCGGACCCAGAACAACTTTCTTCTGTCTCAAC 249

full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match	20.4%	Score 549.6	DB 4	Length 890
Best Local Similarity	85.0%	Pred. No. 1.7e-99		
Matches 663	Conservative 0	Mismatches 109	Indels 8	Gaps 4
QY	893	CTCATACGGCTTCACACCTGGAGTCTTTATAGGCCCTTCCTCAGCGTCACCTCTCTTTAAAC	952	
DB	1	CTCATCAGGCTTCACACCTTCGAGTCTTTCACACCTTCTCTCAGCGTACCTCTTTCACAC	60	
QY	953	C-TAGCATCTACTGAACTCCAGAGGCGCACCCGCTCTCGGCTGATGGGCTCGAGA	1011	
DB	61	CGTCAGCATCTACTGAACTCCAGAGGCGCACTCGTCTTCGCTGATGGGCGCGAGA	120	
QY	1012	GGCAGCGGCGCGAGGCCCTCCGAGGCGCCAGCCCTCACCACCCCA---CGGCTGG	1068	
DB	121	G---GTGTTCCAGAACCCCACTGATGCCCAACCCCTCGCCACTCCAGCTCCCCCAG	177	
QY	1069	CTGCTGGGGCTGTGGCAGAGGGGACCGGGAGGCCATGCGCTGCACAGGTATGGGT	1128	
DB	178	CTGCTGGGGCTGTGGCAAAAGGGGACCGGGAGGCCATGCC-ATGCACAGGTATGGGT	236	
QY	1129	GGGTGAGCGGGCGGTAGCGCTGAGGCGGGGAGGCGACCTCGGGGTGGCGGTGGGG	1188	
DB	237	GGGTGAGGCAAGGCCCTGGTGTTCAGACTGGGGAGGCTGGGCTCGGGGTGGCAGCGTGG	296	
QY	1189	CGGCTCGTGGCTTCACCCACCTCCAGCTCGGCGAGCTCTCGAGGGGCACTGAGAGCC	1248	
DB	297	AGGCGCTGTGCTCTGGCTTACCTTCCAGCTCCGCGAGCTCTTCAAGGGGCACTGAGAGCC	356	
QY	1249	CGGCTCACTCAAGAGGGGCTTCAAGCGCTCGGGCTCTCGGCTCTCGTGAGAGAGCGCAT	1308	
DB	357	ACGCTCACTCAAAGGGGCTTCAAGCCATCAGCGTCTTCAGCGTCTTGGAGAGCGCAT	416	
QY	1309	GAAGATGGTCTCCAGAGCTTCACCCAGCGCTTTCGGCTGTCTCGGAGCAGGAAGTGGC	1368	
DB	417	GAAGATGGTATCCCAAGCATTCACCCAGCGCTTTCGGCTGTCTCGCGGACAGAAGGTAGC	476	
QY	1369	CAAGTCGCTGGCGGTCACTCGTGAGCATCTTTGGCTCTGTGGGCCCACTACACGCTGCT	1428	
DB	477	CAAGTCGCTGGCTATCATCGTGAGCATCTTTGGCTCTGTGGGCCCACTACACATCTCT	536	
QY	1429	GATGATCATCCGGGCGCGCTGCCATGCCACTCGGCTCCCTGACTACTGTGTCAGAACTTC	1488	
DB	537	CATGATCATCCGGGCTGCTTGCCATGCCCACTGCGTCCCCGACTACTGTGTACGAGAGCTC	596	
QY	1489	CTTCTGGCTCTGTGGGCCCAACTCGGCTGTCAACCTGTCTCTTACCTCTGTGGCCACCA	1548	
DB	597	CTTCTGGCTCTGTGGGCCCAACTCGGCGGTCAACCCCGTCTCTTACCCACTGTGGCCACTA	656	
QY	1549	CAGCTTCCGCGGGGCTTCAACCAAGCTGTCTGTCCCCCGAAGCTCAAAATCCAGGCCCA	1608	
DB	657	CAGCTTCCGTAGAGCTTCAACCAAGCTCTTGTCCCCCGAAGCTCAAGTCCAGGCCCA	716	
QY	1609	CAGCTCCCTGGAGCATGTGTGGAAGTAGTGGGCCCAACAGAGGCTCCCTCAGCCACGCT	1668	
DB	717	TGCTCTCCCTGGAGCAGTCTGGAAGTAGCAGCAGTGGCCCAACTTCTTACCGGAGGCGCT	776	

RESULT 6	CB556920	672 bp	mRNA	linear	EST 02-APR-2003
LOCUS	AMGNNUC:URGP1-00001-d6-A	urp1 (14349)	Rattus norvegicus	cDNA clone	
DEFINITION	urp1-00001-d6 5', mRNA sequence.				
ACCESSION	CB556920				
VERSION	CB556920.1	GI:29496320			
KEYWORDS	EST.				
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				

Rattus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source

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1.0012
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="urppl-00001-d6"
/clone.lib="urppl (14349)"
/note="Vector: pSPORT1; Rat G
internal SPORT vector"
source

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ORIGIN

Query Match.	20.1%;	Score 543;	DB 6;	Length 672;
Best Local Similarity	88.1%;	Pred. No. 3.4e-98;		
Matches 591;	Conservative 0;	Mismatches 80;	Indels 0;	Gaps 0;
Qy	182	CCCGACCCGCGCAGGGCCCGCAAGACGAGGCTCCGGGCGGGGGCCCCCTCCGGCGCGC	241	
Db	2	CACGCGTCCGAGAGCGCGCAAGATTAGGTCTACAGCGGGGGGGCCCCACCGGGCCAC	61	
Qy	242	CCAGCTCTCGGCGGGGCGCCTGCCCGCGTCCCGGAGCGCGTAGGCTCGGGGGCCATG	301	
Db	62	CCAGCTCTCGGCGCGTGGCCCTGCCCGGTGTCGCCAGCGGTGTGAGGCTCTCTGGGGCCATG	121	
Qy	302	GAGCGCGCGCGCCCGACGGGCGCGCTGAACGCTTCGGGGGCGCTGGCGGCGATGCGGCG	361	
Db	122	GAGGGCGCGCGCCGACGGGCTGTATGAAACGCGTCGGGCACTCTGGCCGAGAGGGCGCG	181	
Qy	362	CGCGCGGGCGGGCGCGCGGCTTCTCGGCAGCCTGGACCGCGGTGTGTGGCGCGGCTCATG	421	
Db	182	GCTGACGGCGGGCGCGCGGCTTCTCGGCTGCTCGGACCGCTGTCTCGGCTCGGCTCATG	241	
Qy	422	CGCGTGTCTATCGTGGCCACGGTGTGGGCAACGGCGTGTGTATGTCTGCGCTTCGTGGCC	481	
Db	242	CGCGTGTCTATCGTGGCCACAGTACTGGGCAACGGCGTGGTCTATGCTCGGCTTCGTGGCG	301	
Qy	482	GATCGAGCCTCCGACCCAGACAACCTTCTTCTGCTCAACCTCGGCATCTCGGACTTC	541	
Db	302	GATTGAGCCTCCGACCCAGACAACCTTCTTCTGCTCAACCTCGGCACTCTCGGACTTC	361	
Qy	542	CTCGTGGGCGCTTCGTGCATCCCACTGTATGTACCTAGCTGTGTGACAGCGCCCTGAGCC	601	

Db	362	CTCGTGGGTGCCTTCTGCACTCCCATTTGACGTACCCCTATGTGTGACCGGCCGTTGTGACC	421
Qy	602	TTCCGGCCGGGGCCCTCTGCAAGCTGTGGCTGTGTAGTGGACTACCTGTGTGACACTCCTCT	661
Db	422	TTCCGGCCGGGGCCCTCTGCAAGCTGTGGCTGTGTAGTGGACTACCTGTGTGCTCCTCG	481
Qy	662	GCCTTCAACATCGTGTCTCATAGCTACGACCGCTTCTGTCTGGTGCACCGAGCGGTCTCA	721
Db	482	GTCTTCAACATCGTATCTCATCAGCTATGACCGATTCTCTGTCACTCGAGGTGTCTCC	541
Qy	722	TACCGGGCCAGCAGGGTGACACGCGCGGGGCAGTGGGAAGATGCTGTGTGTGGGGTG	781
Db	542	TACAGGGCCAGCAGGGGACACGAGACGGGCCGTTTGGGAAGATGGCACTGGTGTGGGGTG	601
Qy	782	CTGGCTTCTCTGTGTACGGACACGACCATCTGAGCTGGGAGTACCTGTCCGGGGGCAGC	841
Db	602	CTGGCTTCTCTGTGTGTGGGCTGCATCTGAGTTGGGAGTACCTGTCTGGTGGCAGT	661
Qy	842	TCCATCCCCGA	852
Db	662	TCCATCCCCGA	672

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CB154982
LOCUS      CB154982      533 bp      mRNA      linear      EST 29-JAN-2003
DEFINITION K-EST0213081 B2N807043 Homo sapiens cDNA clone B2N807043-31-C05 5',
            mRNA sequence.
ACCESSION  CB154982
VERSION    CB154982.1 GI:28140085
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 533)
AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE     21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 31 row: C column: 05
            High quality sequence stop: 533.
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
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                /sex="M"
                /lab_host="Top10F"
                /clone_lib="B2N807043"
                /note="Organ: Brain; Vector: pCNS-D2; Site 1: EcoRI;
                Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
                bacterial alkaline phosphatase (BAP) and then decapped
                with tabacco acid pyrophosphatase (TAP). The decapped
                intact mRNA was ligated with DNA-RNA linker including
                EcoRI site by treatment of T4 RNA ligase and the first
                strand cDNA was synthesized from oligo dt-selected mRNA by
                priming with dt-tailed vector. The dt-tailed vector was
                adjusted to have about 60nt. The cDNA vector was
                circularized with E. coli DNA ligase after digestion of
                EcoRI which site is also included in vector. An RNA strand
                converted to a DNA strand by Okayama-Berg method. The
                obtained cDNA vectors were used for transformation of
                competent cells E. coli Top10F by electroporation method.
                The cDNA libraries constructed by this method are
                full-length enriched cDNA library."

FEATURES             source
    source
ORIGIN
    Query Match      19.3%; Score 522; DB 6; Length 533;
    Best Local Similarity 99.8%; Pred. No. 5.4e-94;
    Matches 533; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1416 CATACACGCTGCTGATGATCATCCGGCGCGCTGCCATGGCCACTGCTCCCTGACTACT 1475
DB 1 CATACACGCTGCTGATGATCATCCGGCGCGCTGCCATGGCCACTGCTCCCTGACTACT 60

QY 1476 GGTAGAAACCTCTTCTGGCTCTGTGGGCAACTCGGCTGTCAACCTGTCCTTACC 1535
DB 61 GGTAGAAACCTCTTCTGGCTCTGTGGGCAACTCGGCTGTCAACCTGTCCTTACC 120

QY 1536 CTCCTGTCACACAGCTTCGCGCGGCTTACCAAGCTGCTGCGCCCGCAGAGCTCA 1595
DB 121 CTCCTGTCACACAGCTTCGCGCGGCTTACCAAGCTGCTGCTGCGCCCGCAGAGCTCA 180

QY 1596 AAATCCAGCCCAACAGCTCCCTGGAGCACTGCTGGAAGTAGTGCCGCCACAGAGCTCC 1655
DB |||||
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181 AAATCCAGCCCAACAGCTCCCTGGAGCACTGCTGGAAGTAGTGCCGCCACAGAGCTCC 240
QY |||||
1656 CTCAGCCACGCTCTCTCAGCCCGAGGCTCTCTCTGGGCACTCTGGCCCTGCTGCCCCCTACCC 1715
DB |||||
241 CTCAGCCACGCTCTCTCAGCCCGAGGCTCTCTCTGGGCACTCTGGCCCTGCTGCCCCCTACCC 300
QY |||||
1716 GGCTCGTTTCCCCCAGGCGGTGAGCCCGCCGCTGTCTGTGGCCCTCTCTTAATGCCACGGCA 1775
DB |||||
301 GGCTCGTTTCCCCCAGGCGGTGAGCCCGCCGCTGTCTGTGGCCCTCTCTTAATGCCACGGCA 360
QY |||||
1776 GCCACCTGTCATGAGCGGCTCTTCTGGGTGGCCAGAGGGCCCTCCTCAGTGGTGGACT 1835
DB |||||
361 GCCACCTGTCATGAGCGGCTCTTCTGGGTGGCCAGAGGGCCCTCCTCAGTGGTGGACT 420
QY |||||
1836 GGAGGCTGGGTGGCGGCGCTGCCCCCAGCTTCTGGCTCCACCGGGAGGAGGACAGTCTG 1895
DB |||||
421 GGAGGCTGGGTGGCGGCGCTGCCCCCAGCTTCTGGCTCCACCGGGAGGAGGACAGTCTG 479
QY |||||
1896 GAGGTCCCGACAGATGCTGCCACCCCTGCTGGTGGCCACCTTTCGCAGTTACT 1949
DB |||||
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RESULT 8
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LOCUS      CN423054      716 bp      mRNA      linear      EST 16-MAY-2004
DEFINITION 17000424504731 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CN423054
VERSION    CN423054.1 GI:47410648
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 716)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Lebkowski,J and Stanton,L.W.
            Transcription characterization elucidates signaling networks that
            control human ES cell growth and differentiation
            Nat. Biotechnol. 22 (6), 707-716 (2004)
            Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8638
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 716 Std Error: 0.00.
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                /note="G1igo dt primed, full-length enriched cDNA library
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FEATURES             source
    source
ORIGIN
    Query Match      19.1%; Score 516; DB 7; Length 716;
    Best Local Similarity 100.0%; Pred. No. 8.8e-93;
    Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 548 GGCGCTTCTGCATCCCACTGTATGTACCTTACCTGTGACAGCGCGCTGCACCTTCGGC 607
DB 201 GGCGCTTCTGCATCCCACTGTATGTACCTTACCTGTGACAGCGCGCTGCACCTTCGGC 260
QY 608 CGGGGCTCTGCAAGCTGTGGCTGGTAGTGACTCTCTGTGTGACCTCTCTGCTTC 667
DB 261 CGGGGCTCTGCAAGCTGTGGCTGGTAGTGACTCTCTGTGTGACCTCTCTGCTTC 320
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QY 668 AACATGCTCATCAGCTACGACCGCTTCCTGTCGGTCCACCGAGCGGTCTCATACCGG 727
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Db 321 AACATGCTCATCAGCTACGACCGCTTCCTGTCGGTCCACCGAGCGGTCTCATACCGG 380
|
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|
QY 728 GCCCAGAGGCTGACACCGCGGGGCGAGTCGTCGGTCCACCGAGCGGTCTCATACCGG 787
|
|
|
Db 381 GCCCAGAGGCTGACACCGCGGGGCGAGTCGTCGGTCCACCGAGCGGTCTCATACCGG 440
|
|
|
QY 788 TTCTCTGCTACCGGACACCGCGGTTCCTGAGCTGGGAGTACCTGTCCGGGGGCGAGCTCCATC 847
|
|
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Db 441 TTCTCTGCTACCGGACACCGCGGTTCCTGAGCTGGGAGTACCTGTCCGGGGGCGAGCTCCATC 500
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QY 848 CCGAGAGGCGACCTGCTATCGGAGTTCTTCTCAACTGCTATCTTCTCACTACCGGCTTCC 907
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Db 501 CCGAGAGGCGACCTGCTATCGGAGTTCTTCTCAACTGCTATCTTCTCACTACCGGCTTCC 560
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QY 908 ACCCTGGAGTCTTTACGCGCTTCTTCAAGCTGCTTCTTCACTACCGGCTTCC 967
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Db 561 ACCCTGGAGTCTTTACGCGCTTCTTCAAGCTGCTTCTTCACTACCGGCTTCC 620
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QY 968 AACATCCAGAGCGCACCGCGCTCCGCTGGGCTCGAGAGCGAGCGCGCGCGCGAG 1027
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Db 621 AACATCCAGAGCGCACCGCGCTCCGCTGGGCTCGAGAGCGAGCGCGCGCGCGAG 680
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QY 1028 CCCCCTCCGAGGCGCGAGCGCTTCAACACCGCGCGCGAG 1063
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Db 681 CCCCCTCCGAGGCGCGAGCGCTTCAACACCGCGCGAG 716
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RESULT 9
BE783826 910 bp mRNA linear EST 20-OCT-2000
LOCUS 601471053F1 NTH_MGC_67 Homo sapiens cDNA clone IMAGE:3874260 5',
RNA sequence.
ACCESSION BE783826
VERSION BE783826.1 GI:10205024
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9631 row: i column: 13
High quality sequence stop: 601.
FEATURES
Location/Qualifiers
1..910
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3874260"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 67"
/site="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 17.7%; Score 476.6; DB 2; Length 910;

Best Local Similarity 89.1%; Pred. No. 7.le-85;
Matches 632; Conservative 0; Mismatches 54; Indels 23; Gaps 10;
QY 1177 TGGCGGTGGGGCGCGCTCGTGGCTTCAACCACTCCAGCTCCGGCAGCTCTCTCGAGGGG 1236
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Db 181 CAGGAAAGTGGCCAAAGTGGTGGCGCTCATCTGAGCATCTTTGGGCTCTGTGGGCGCC 240
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QY 1417 ATACACGCTGTGATGATCATCCGGGCGCGCTGCCATGGCCACTGCGTCCCTGACTACTG 1476
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|
Db 241 ATACACGCTGTGATGATCATCCGGGCGCGCTGCCATGGCCACTGCGTCCCTGACTACTG 300
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QY 1477 GTACGAAACCTCTTCTGGCTCTGTGGGCGCGCTGCCATGGCCACTGCGTCCCTGACTACTG 1536
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Db 301 GTACGAAACCTCTTCTGGCTCTGTGGGCGCGCTGCCATGGCCACTGCGTCCCTGACTACTG 360
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RESULT 10
CN335777
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ACCESSION CN335777
VERSION CN335777.1 GI:47335711
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 466)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
```

230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@eron.com
Insert Length: 466 Std Error: 0.00.
Location/Qualifiers

FEATURES

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/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
/clone_lib="GRN ES"
/note="oligo dt primed, full-length enriched cDNA library from underidentified hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Query Match 16.9%; Score 455; DB 7; Length 466;
Best Local Similarity 99.8%; Pred. No. 1.4e-80;
Matches 466; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1593 TCAAAATCAGCCACAGCTCCCTGGAGCACTGCTGGAAGTACTGGCCACACAGAGCC 1652
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QY 1713 CCCGCTGTTCCTCCAGGGTGAGCCCGCGCTCTGTGGCCCTCTCTTAATGCCACG 1772
Db 121 CCCGCTGTTCCTCCAGGGTGAGCCCGCGCTCTGTGGCCCTCTCTTAATGCCACG 180
QY 1773 GCAGCCACCTGCCATGAGGCGCTTCCTGGTTGGCCAGAGGCGCCCTCACTGGCTGG 1832
Db 181 GCAGCCACCTGCCATGAGGCGCTTCCTGGTTGGCCAGAGGCGCCCTCACTGGCTGG 240
QY 1833 ACTGAGGCTGGTGGCGCGCTCGCCGCCACATTCGTGCTCCACCGGGAGGACAGT 1892
Db 241 ACTGAGGCTGGTGGCGCGCTCGCCGCCACATTCGTGCTCCACCGGGAGGACAGT 299
QY 1893 CTGGAGTCCACAGACATGCTGCCACCCCTCTGCTGGTCCACCCCTTCGCACTTACTGCT 1952
Db 300 CTGGAGTCCACAGACATGCTGCCACCCCTCTGCTGGTCCACCCCTTCGCACTTACTGCT 359
QY 1953 TGGTGTCTTCCAAAGCAAGCACCTGGGTGTGCTCCAGGCTTCCTGCGCTAGCAGTTTG 2012
Db 360 TGGTGTCTTCCAAAGCAAGCACCTGGGTGTGCTCCAGGCTTCCTGCGCTAGCAGTTTG 419
QY 2013 CTTCTGCAGTGCACACACCTTGCACACCCCTTGCACACACCTTGCACAC 2059
Db 420 CTTCTGCAGTGCACACACCTTGCACACCCCTTGCACACACCTTGCACAC 466

RESULT 11

CO403631
LOCUS
DEFINITION CO403631 842 bp mRNA linear EST 01-JUL-2004
AGENCY 27526928 NIH MGC 254 Rattus norvegicus cDNA clone
IMAGE:7315203 5', mRNA sequence.
ACCESSION CO403631
VERSION CO403631.1 GI:49585547
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 842)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH
Blc9. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LAM15369 row: b column: 01
High quality sequence stop: 637.
Location/Qualifiers

FEATURES

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/db_xref="taxon:10116"
/clones="IMAGE:7315203"
/sex="both"
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/lab_host="DH10B Tona"
/clone_lib="NIH MGC 254"
/note="Organ: brain/CNS; Vector: pExpress-1; Site: 1: EcoRV; Site 2: NotI; RNA obtained from brain tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer: 5'-PGACTAGTCTAGTCCGAGGCGGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 2.18 kb. This primary library is not normalized (normalized library is NIH MGC 255) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library"

ORIGIN

Query Match 15.9%; Score 429.6; DB 7; Length 842;
Best Local Similarity 83.7%; Pred. No. 1.9e-75;
Matches 538; Conservative 0; Mismatches 90; Indels 15; Gaps 4;
QY 14 GGCTGCAGGTCGACCGGACCGGCTCAGGCTCGGCTCTCTCCGCTCAGCAGCGG 73
Db 39 GGGTGCAACGACGACCGGCGGCGCTGAGCT-CGGCTTGTCTCTCGCTCAGCAGCGG 97
QY 74 CGCTGCCGCGCCCACTGGGCTCGGA-TCCGCGCCCGGCGCCCTCGGCACCGGCT----- 126
Db 98 CGCGCGCGCCCACTCGCTCAGATTCGACACACGACCGCCCTCTGGATCGCCCTCTGG 157
QY 127 -----GCTCTGGCCCGGCGCCCGGCGCCCGGACCATGCGCTGGGCGCGCCCGGCGGAA 180
Db 158 ACTCTAGCCGCGGCTCTTGTCTCCGACCCCGGCGGACCATGCTCCGCGCGCCCGCC-CGGAAA 216
QY 181 ACCGACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 217 ACCGCGCTGGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 276
QY 241 CCCAGCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 277 CCCAGCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 336
QY 301 GGAGCGG 360
Db 337 GGAGCGG 396
QY 361 GGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Db 397 GGCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 456
QY 421 GGCGCTGCTCATCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Db 457 GGCGCTGCTCATCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 516

Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

ORIGIN

Query Match	14.3%	Score 386;	DB 2;	Length 409;
Best Local Similarity	98.5%;	Pred. No. 9.6e-67;		
Matches 400;	Conservative 0;	Mismatches 5;	Indels 1;	Gaps 17;
QY	2127	GCCTGGCCCTTTACACCCCTCTTCCACCAACTCTCTCTGCCCCCAAAAGTGTCAAGGGGC	2186	
DB	5	GGCCTGGCCTTTACCCCTCTTCCACCAACTCTCTCTGCCCCCAAAAGTGTCAAGGGGC	64	
QY	2187	CCTAGGAACCTCGAAGCTGTCTCTGCTGCTTTTCCATTCTGGGTGTTTTCAGAAAGATGAAG	2246	
DB	65	CCTAGGAACCTCGAAGCTGTCTCTGCTGCTTTTCCATTCTGGGTGTTTTCAGAAAGATGAAG	124	
QY	2247	AAGAAACAATGCTGTGAACTTGATGTTCTGTGGATGTTTAAATCAAGAGAGACAAAAATTG	2306	
DB	125	AAGAAACAATGCTGTGAACTTGATGTTCTGTGGATGTTTAAATCAAGAGAGACAAAAATTG	184	
QY	2307	CTGAGGAGCTCAGGGCTGGATTGGCAGGTGTGGGCTCCACGCCCTCTCCCTCCCGCTAA	2366	
DB	185	CTGAGGAGCTCAGGGCTGGATTGGCAGGTGTGGGCTCCACGCCCTCTCCCTCCCGCTAA	244	
QY	2367	GGCTTCGGGCTGAGCTGTGCAGCTGCTTGTGCCACCCCGCTCTGGGCTCACACGAC	2426	
DB	245	GGCTTCGGGCTGAGCTGTGCAGCTGCTTGTGCCACCCCGCTCTGGGCTCACACGAC	304	
QY	2427	CCTGTTGGCCCAAGCTGCCCCGGGCACCTCTGTTTGTCTACCCAGGACCTCTGGGGGTTGT	2486	
DB	305	CCTGTTGGCCCAAGCTGCCCCGGG-CACCTCTGTTTGTCTACCCAGGACCTCTGGGGGTTGT	363	
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RESULT 15	BF567596	LOCUS	BF567596	499 bp	mRNA	linear	EST 12-DEC-2000
DEFINITION	UI-R-B00-agr-c-06-0-UI.r1 UI-R-B00 Rattus norvegicus cDNA clone						
	UI-R-B00-agr-c-06-0-UI 5', mRNA sequence.						

ACCESSION	BF567596	
VERSION	BF567596.1	GI:11677326
KEYWORDS	EST.	
SOURCE	<i>Rattus norvegicus</i> (Norway rat)	
ORGANISM	<i>Rattus norvegicus</i>	
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	Mammalia; Eutheria; Rodentia;	
	Sciurognathi; Muridae; Murinae;	
	<i>Rattus</i> .	
	Craniata; Vertebrata; Euteleostomi;	

1 (bases 1 to 499)
 Bonaldo M.F., Lennon G. and Soares M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 8889548
 Contact: Soares MB

Contact: Soares, M.B.
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LNLN (info@image.llnl.gov). IMAGE ID= 1796445
Seq primer: M13 Forward.

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Location/Qualifiers
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/mol type="mRNA"
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/strain="Sprague-Dawley"
 /db xref="taxon:10116"
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 /dev stage="adult"
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 /notes="Vector: p773D-Pac (Pharmacia) with a modified
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 (UI-R-B00) is a subtracted library derived from a mixture
 of the following tissues: thalamus, cerebellum,
 hypothalamus, medulla, pons, midbrain, cerebral
 corpus striatum and hippocampus. For a detailed
 description of the library from which this clone was
 derived, please visit our web site at
 ratest.eng.utoro.edu. The subtraction has been previously
 described in (Bonaldo, Lennon and Soares, Genome Research
 6:791-806, 1996)."

ORIGIN

Query Match	13.8%	Score	371.2	DB	2	Length	499
Best Local Similarity	90.0%	Pred. No.	9e-64				
Matches	397	Conservative	0	Mismatches	44	Indels	0
Gaps	0						
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Qy	608	CGGGGGCTCTGC	AAAGCTGTGGCTGTGGTAGTGGACTACTGCTGTGTGCACCTCCTCTGCGCTTC	667			
Db	119	CGGGGGCTCTGC	AAAGCTGTGGCTGTGGTAGACTACTACTGTGTGGCTCCTCGGTCTTC	178			
Qy	668	AACATCGTGCTC	ATCAGCTACGACCGCTTCCTGTCGGTCAACCGAGCGGTCTCATACCG	727			
Db	179	AACATCGTACT	CATCAGCTATGACCGATTCTCTCAGTCACTCGAGCTGCTCTCTACAGG	238			
Qy	728	GCCACGAGGGTGA	CACGGCGGGGAGTCGGAAAGATGCTGCTGTGTGGGTGCTGGCC	787			
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Qy	788	TTCTCTGCTACG	GACGCCATCTGTAGCTGGAGTACCTGTCCGGGGGACGCTCCATC	847			
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Qy	848	CCGAGGGCCACT	GCTATGCCGAGTTCTTCTCAAACTGGTACTTCTCTCATCACGGCTTCC	907			
Db	359	CCGAGGGCCACT	GCTATGCTGAGTTCTTCTCAAACTGGTACTTCTCTCATCACGGNCTCC	418			
Qy	908	ACCCTGGAGTTC	TTTATACGCCCTTCTCAGCGTCACCTTCTTTAAACCTCAGCATCTACCTG	967			
Db	419	ACCCTGGAGTTC	TTTACGCCCTTCTCAGCGTTACCTTCTTCAACCTCAGCATCTACCTG	478			
Qy	968	AACATCAGAGG	CGGCACCCGC	988			
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Job time : 8905.2 secs

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Db      1021 TCCAGAGCTTACCCAGCGCTTTCGGCTGTCTCGGGAAGAAAGTGGCCAAAGTGGTG 1080
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QY      1321 GAGCACTGCTGGAAG 1335
Db      1321 GAGCACTGCTGGAAG 1335
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RESULT 2

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BD235873
LOCUS      BD235873
DEFINITION Isolated DNA encoding human H3 histamine receptor.
ACCESSION  BD235873
VERSION    BD235873.1 GI:33045643
KEYWORDS   JP 2002526049-A/6.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 1335)
AUTHORS   Labenberg,T.W., Erlander,M., Huber,A. and Piatei,J.
TITLES    Isolated DNA encoding human H3 histamine receptor
JOURNAL   Patent: JP 2002526049-A 6 20-AUG-2002;
          ORTHO MCNEIL PHARMACEUTICAL INC
COMMENT    OS Artificial Sequence
          PN JP 2002526049-A/6
          PD 20-AUG-2002
          PF 07-OCT-1998 JP 2000573370
          PI TIMOTHY W LABENBERG, MARK ERLANDER, ARNE HUBER, JIYAYASYURY PI
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A61P25/16
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PC C12N1/15,
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FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 7.7e-178;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGAGAGCGCGCGCGCGCGCGCGCTGAAACGCTTCGGGGCGCTGGCGGCGATGCG 60
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RESULT 4
AR135732
LOCUS      AR135732          2699 bp      DNA      linear      PAT 16-JUN-2001
DEFINITION Sequence 5 from patent US 6136559.
ACCESSION AR135732
VERSION   AR135732.1  GI:14476404
KEYWORDS  'Unknown.'
SOURCE    'Unknown.'
ORGANISM  'Unclassified.'
REFERENCE 1 (bases 1 to 2699)
AUTHORS   Lovenberg,T.W., Ezrlan,M., Huvar,A. and Pyati,J.
TITLE     DNA encoding as human histamine receptor of the H3 subtype
JOURNAL   Patent: US 6136559-A 5 24-OCT-2000;
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Best Local Similarity 100.0%; Pred. No. 6,7e-178;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGGAGCGCGCGCGCGCGCGCGCGCTGAAACGCTTCGGGGCGCGTGGCGGCGATGCG 60
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Qy      841  GCGTAGGCGCTGAGGCGGGGAGCGGACCTTCGGGGGTGGGGGTGGGGGGCGCTCCGTC 900
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LOCUS BD235872 2699 bp DNA linear PAT 17-JUL-2003

DEFINITION Isolated DNA encoding human H3 histamine receptor.

ACCESSION BD235872

VERSION BD235872.1 GI:33045642

KEYWORDS JP 2002526049-A/5.

SOURCE synthetic construct

ORGANISM other sequences: artificial sequences.

REFERENCE 1 (bases 1 to 2699)

AUTHORS Labenberg,T.W., Erlander,M., Huber,A. and Platei,J.

TITLE Isolated DNA encoding human H3 histamine receptor

JOURNAL Patent: JP 2002526049-A 5 20-AUG-2002;

ORFHO MCNEIL PHARMACEUTICAL INC

COMMENT OS Artificial Sequence

PN JP 2002526049-A/5

PD 20-AUG-2002

PF 07-OCT-1998 JP 2000573370

PI TIMOTHY W LABENBERG, MARK ERLANDER, ARNE HUBER, JIYAYASYURY PI

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PC C12N15/09, A61K38/00, A61K45/00, A61P3/04, A61P3/10, A61P9/06, PC

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PC A61P25/19, A61P25/22, A61P25/24, A61P25/28, C07K14/705, C07K16/28,

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PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/02, C12Q1/68 PC

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CC Description of Artificial Sequence: CDNA

FH Key Location/Qualifiers

FT source 1..2699

FT /organism='Artificial Sequence'.

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Best Local Similarity 100.0%; Pred. No. 6.7e-178;

Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 299 ATGGAGCGCGCGCGCGCGCGCGCGCTGAAACGCTTCGGGGCGCGTGGCGGGCGATCGG 358

Qy 61 GCGGCGGGCGGGCGCGCGCGCTTCCTCGGCGAGCTTGACCGCGGTGCTGCGCGGCTC 120

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	Dd	1139	GCGTAGGGCGCTCAGGCGGGGAGGCGACCCTCGGGGTGGGGTGCGGCTCCGCT	1198
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	Dd	1199	GCTTCACCCACCTCCAGCTCCGGCAGCTCTCGAGGGGCACTGACAGAGCGCGCTCACCTC	1258
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	Dd	1439	CGGGCGCTGCGCATGCGCCACTGCGTCTGCTGGGCCCCATACACGCTGCTTGGCTC	1498
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	Qy	1261	CGGGCGCTTACCAAAGCTGCTGCCCCCAGAGAGCTCAAAATCCAGCCCCACAGCTTCCG	1320
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	REFERENCE	1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
	AUTHORS	Burmer, G.C., Roush, C.L. and Brown, J.P.		
	TITLE	Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides		
	JOURNAL	Patent: WO 02061087-A 548 08-AUG-2002;		
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	Best Local Similarity	100.0%; Pred. No. 6.7e-178;		
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	Qy	481	GTGCTGCGCTTCTGCTGTAGGACACCACTCTGAGCTGGGAGTACCTGTCGCGGGGC	540
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DEFINITION E39824 2050 bp DNA linear PAT 31-JAN-2002
receptor protein.
ACCESSION E39824
VERSION E39824.1 GI:18627105
KEYWORDS JP 2000189171-A/19.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2050)
AUTHORS Itaya,K., Takimura,T., Nakamura,T., Kobayashi,M., Tana,K.,
Hidaka,Y. and Ota,M.
TITLE Novel guanosine triphosphate (GTP)-binding protein-conjugate
JOURNAL BANYU PHARMACEUT CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2000189171-A/19
PD 11-JUL-2000
PF 25-MAY-1999 JP 1999145661
PR 25-DEC-1998 WO PCTJP9805967
PI KEI ITAYA, TETSUO TAKIMURA, TAKAO NAKAMURA, MASAHIKO KOBAYASHI,
PI KENICHI TANAKA,
PI YUSUKE HIDAKA, MASAKI OTA
PC C12N15/09, A61K45/00, C07K14/705, C12N1/15, C12N1/19, C12N1/21, PC
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KEYWORDS
SOURCE
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Unclassified.
REFERENCE
1 (bases 1 to 2050)
AUTHORS
Itadani,H., Takimura,T., Nakamura,T., Kobayashi,M., Tanaka,K.-I.,
Hidaka,Y. and Ohta,M.
TITLE
Guanosine triphosphate (GTP) binding protein-coupled receptor
proteins
JOURNAL
Patent: US 6750322-A 21 15-JUN-2004;
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Best Local Similarity 99.9%; Pred. No. 1.6e-177;
Matches 1333; Conservative. 0; Mismatches 1; Indels 0; Gaps 0;

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REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1335)				
TITLE	Goodearl,A.D.J. and Glucksmann,M.Alexandra. Methods for detecting nucleic acid molecules encoding a member of the muscarinic family of receptors				
JOURNAL	Patent: US 6093545-A 3 25-JUL-2000;				
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 04:43:59 ; Search time 712.507 Seconds
(without alignments)

11091.610 Million cell updates/sec

Title: US-10-727-021-6

Perfect score: 1335

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Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	1335	100.0	2699	3	Aaa09061 Human his
7	1335	100.0	2699	4	Aac62365 Complete
8	1335	100.0	2699	6	Abn84882 Human his
9	1335	100.0	2699	8	Abz42533 Human his
10	1335	100.0	2699	9	Acc59394 Human his
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13	1335	100.0	2699	13	Adr31456 Human his
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16	1332.4	99.8	2050	3	Aaa70637 Human G-p
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26	1206.6	90.4	1293	9	AAL59982	Aal59982 Human H3
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ALIGNMENTS

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AC AAA09062;

DT 10-AUG-2000 (first entry)

XX Human histamine H3 receptor open reading frame.

DE histamine H3 receptor; biogenic amine receptor homologue; ss.

XX Homo sapiens.

PN WO200020011-A1.

PD 13-APR-2000.

XX 07-OCT-1998; 98WO-US021090.

XX 07-OCT-1998; 98WO-US021090.

XX (ORTH) ORTHO-MCNEIL PHARM INC.

XX Lovenberg TW, Erlander M, Huvar A, Pyati J;

DR WPI: 2000-303632/26.

DR P-PSDB; AAY92218.

PT Novel human histamine H3 receptor polynucleotides and polypeptides used in methods to identify modulators of receptor activity.

PS Claim 2; Fig 2; 54pp; English.

XX The cDNA encodes the human histamine H3 receptor. The polypeptide contains the seven conserved hydrophobic domains and specific residues conserved in biogenic amine receptors. The human histamine H3 receptor polynucleotides and polypeptides are used in methods to screen for modulators of receptor activity (claimed). Such agonists and antagonists may prove useful as research tools or may be used as therapeutics to treat disorders directly or indirectly involving histamine receptors (claimed). The characterization of the polynucleotide is useful for forensic analysis, diagnostic applications, and epidemiological studies

Db 1439 CGGGCGCGCTGCATGGCCACTGCGCTGCTGCTACTGTGTACGAAACCTCTCTTGGGCTC 1498
Qy 1201 CTGTGGGCAACTCGGCTGTCAACCTGTCTCTACCTCTGTGTGCACACAGCTTCGC 1260
Db 1499 CTGTGGGCAACTCGGCTGTCAACCTGTCTCTACCTCTGTGTGCACACAGCTTCGC 1558
Qy 1261 CGGGCTTCCACCAAGCTGCTGTGCGCCCGCCAGAGCTCAAAATCCAGCCCGCCACAGCTCCCTG 1320
Db 1559 CGGGCTTCCACCAAGCTGCTGTGCGCCCGCCAGAGCTCAAAATCCAGCCCGCCACAGCTCCCTG 1618
Qy 1321 GAGCACTGCTGAAG 1335
Db 1619 GAGCACTGCTGAAG 1633

RESULT 9

ABZ42533

ID ABZ42533 standard; DNA; 2699 BP.

XX

AC ABZ42533;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human histamine H3 receptor nucleotide SRQ ID NO:548.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft-versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burner GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

XX

DR P-PSDB; ABP81687.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX

PS Disclosure; Fig 1; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell

Db 1079 TCTGCGAAGAGGACGCGGAGGCGCATGCGCGTGCAAGGTATGGGTGAGGGG 1138
QY 841 GCCGTAGGCGCTGAGGCCGCGGAGGCGACCCCTCGGGGTGGCGGTGGGGCGGCTCCGCG 900
Db 1139 GCCGTAGGCGCTGAGGCCGCGGAGGCGACCCCTCGGGGTGGCGGTGGGGCGGCTCCGCG 1198
QY 901 GCTTACCACCTCTCAGCTCCGCGAGCTCTCGAGGGGCACTGAGAGGCGCGCTCACTC 960
Db 1199 GCTTACCACCTCTCAGCTCCGCGAGCTCTCGAGGGGCACTGAGAGGCGCGCTCACTC 1258
QY 961 AGAGGGGCTCAAGCGCTCGGGCTCTCGGGCTCTCGGGAGGCGATGAAGATGGT 1020
Db 1259 AAGAGGGGCTCAAGCGCTCGGGCTCTCGGGCTCTCGGGAGGCGATGAAGATGGT 1318
QY 1021 TCCAGAGCTTCAACCCAGCGCTTTCGGCTGTCTCGGGACAGAAAGTGGCCAAAGTCGCTG 1080
Db 1319 TCCAGAGCTTCAACCCAGCGCTTTCGGCTGTCTCGGGACAGAAAGTGGCCAAAGTCGCTG 1378
QY 1081 GCCGTATCGTCAGCATCTTTCGGCTGTCTCGGGGCCCCATACACGCTGCTGATGATCATC 1140
Db 1379 GCCGTATCGTCAGCATCTTTCGGCTGTCTCGGGGCCCCATACACGCTGCTGATGATCATC 1438
QY 1141 CGGGCGGCTCGCATGGGCACTGGCTCCCTGACTACTGTAGAAACCTCTTCTGGGCTC 1200
Db 1439 CGGGCGGCTCGCATGGGCACTGGCTCCCTGACTACTGTAGAAACCTCTTCTGGGCTC 1498
QY 1201 CTGTGGGCGCACTCGGCTGTCAACCTGTCTACCTCTGTGCGCCACACAGCTTCGCG 1260
Db 1499 CTGTGGGCGCACTCGGCTGTCAACCTGTCTACCTCTGTGCGCCACACAGCTTCGCG 1558
QY 1261 CGGGCTTTCACCAAGCTGTCTGCGGCCCCAGAGCTCAAAATCCAGCCCCACAGCTCCCTG 1320
Db 1559 CGGGCTTTCACCAAGCTGTCTGCGGCCCCAGAGCTCAAAATCCAGCCCCACAGCTCCCTG 1618
QY 1321 GAGCACTGCTGAAG 1335
Db 1619 GAGCACTGCTGAAG 1633

RESULT 10

ACCS9394

ID ACCS9394 standard; DNA; 2699 BP.

XX AC

XX AC

XX AC

XX AC

DT 28-AUG-2003 (first entry)

XX Human histamine H3 receptor nucleotide sequence.

XX Human;

KW Human; histamine H3 receptor; receptor modulator; gene; ds; agonist;

KW nootropic; neuroprotective; cerebroprotective; cardiant; antiasthmatic;

KW immunomodulator; gastrointestinal; antiallergic; antidiabetic;

KW antiinflammatory; hypotensive; antiarrhythmic.

XX OS

XX Homo sapiens.

XX PN

XX WO2003044059-A1.

XX PD

XX 30-MAY-2003.

XX PF

XX 15-NOV-2001; 2001WO-US045313.

XX PR

XX 15-NOV-2001; 2001WO-US045313.

XX XX

XX (ORTH) ORTHO-MCNEIL PHARM INC.

XX PA

XX Lovenberg T;

XX PI

XX WPI; 2003-457595/43.

XX DR

XX Identifying agonists of recombinant human histamine H3 receptor protein

PT activity, useful for diagnosing and treating H3 receptor-related

PT

disorders, such as nervous system disorders, asthma, allergy, hypertension and diabetes.

Example 1; Fig 1; 55pp; English.

The present invention relates to a method of identifying compounds that are agonists of recombinant human histamine H3 receptor protein activity, comprising combining a compound suspected of being an antagonist of human histamine H3 receptor protein activity with recombinant human histamine H3 receptor protein, and measuring an agonistic effect of the compound on the recombinant human histamine H3 receptor protein. The methods and compositions of the present invention are useful for diagnosing and treating human histamine H3 receptor-related disorders, such as central and peripheral nervous system disorders (depression, anxiety, psychoses, Parkinson's disease, Alzheimer's disease, dementia and tardive dyskinesia), asthma, allergy, diabetes mellitus, inflammation, immune, cardiovascular (hypertension, and arrhythmia) and gastrointestinal disorders. The present sequence is the coding sequence of the human histamine H3 receptor

Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;

Query Match 100.0%; Score 1335; DB 9; Length 2699;

Best Local Similarity 100.0%; Pred. No. 3.3e-217;

Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGCGCGCGCCCGACGCGGCGCTGAAACGCTTCGGGGGCGCTGGCGGCGATGCG 60

Db 299 ATGAGAGCGCGCGCCCGACGCGGCGCTGAAACGCTTCGGGGGCGCTGGCGGCGATGCG 358

QY 61 GCGGCGGCGGCGGCGCGCGGCTTCTCGGCAGCGCTTGACCGCGGTGTGCCCGGCTC 120

Db 359 GCGGCGGCGGCGGCGCGGCTTCTCGGCAGCGCTTGACCGCGGTGTGCCCGGCTC 418

QY 121 ATGGCGCTGCTCATCGTGGCCACGCTGTGGGCAACGCGCTGATGCTCCGCTTCGTC 180

Db 419 ATGGCGCTGCTCATCGTGGCCACGCTGTGGGCAACGCGCTGATGCTCCGCTTCGTC 478

QY 181 GCCGACTCGAGCTCCGCAACCCAGAAACAATCTTCTTCTGCTCAACTCGCCATCTCCGAC 240

Db 479 GCCGACTCGAGCTCCGCAACCCAGAAACAATCTTCTTCTGCTCAACTCGCCATCTCCGAC 538

QY 241 TTCTCTGTGGCGCTTCTGTCATCCCACTGTATGATACCTACGTGTGACAGCGCGCTGG 300

Db 539 TTCTCTGTGGCGCTTCTGTCATCCCACTGTATGATACCTACGTGTGACAGCGCGCTGG 598

QY 301 ACCTTGGCGCGGCGCTCTGCAAGCTGTGGTAGTGGACTACCTGCTGTGACCTCC 360

Db 599 ACCTTGGCGCGGCGCTCTGCAAGCTGTGGTAGTGGACTACCTGCTGTGACCTCC 658

QY 361 TCTGCTTCAACATCGTCTCATAGCTACGACCGCTTCTCTGCTCAACCCGAGCGGTC 420

Db 659 TCTGCTTCAACATCGTCTCATAGCTACGACCGCTTCTCTGCTCAACCCGAGCGGTC 718

QY 421 TCATACCGGCGCCAGCAGGCTGACACGCGGCGGCGAGTGCAGGAATGCTGTGGTGG 480

Db 719 TCATACCGGCGCCAGCAGGCTGACACGCGGCGGCGAGTGCAGGAATGCTGTGGTGG 778

QY 481 GTGCTGGCGCTTCTGCTGTACGACACGACGATCTCTGAGCTGGAGTACTCTGCGGGGCG 540

Db 779 GTGCTGGCGCTTCTGCTGTACGACACGACGATCTCTGAGCTGGAGTACTCTGCGGGGCG 838

QY 541 AGCTCCATCCCGAGGGGCGCTGCTATCCGAGTTCTTCTCAACTGGTACTTCTCATC 600

Db 839 AGCTCCATCCCGAGGGGCGCTGCTATCCGAGTTCTTCTCAACTGGTACTTCTCATC 898

QY 601 ACGGCTTCCACCTGGAGTCTTCTTACGCGCTTCTCTCAGCGTCACTTCTTTAACTTCAGC 660

Db 899 ACGGCTTCCACCTGGAGTCTTCTTACGCGCTTCTCTCAGCGTCACTTCTTTAACTTCAGC 958

QY 661 ATCTACCTGAACATCCAGAGGCGCAACCGCTTCCGGCTGGATGGGGCTCGAGAGGCGGCC 720

Db 959 ATCTACCTGAACATCCAGAGGCGCAACCGCTTCCGGCTGGATGGGGCTCGAGAGGCGGCC 1018

Qy	721	GGCCCCGAGCCCTCCGAGGCCAGCCTCACCACCCCACCGCCTGCTGCTGGGGC	780
Db	1019	GGCCCCGAGCCCTCCGAGGCCAGCCTCACCACCCCACCGCCTGCTGCTGGGGC	1078
Qy	781	TGCTGGCAGAGGGGCGAGGGGAGCCATGCCCTGCACAGGTATGGGTGGGTGAGGCG	840
Db	1079	TGCTGGCAGAGGGGCGAGGGGAGCCATGCCCTGCACAGGTATGGGTGGGTGAGGCG	1138
Qy	841	GCCGTAGCGCTGAGAGCGGGGAGCGACCTCCGGGGTGGCGGTGGGGCGGCTCCGCTG	900
Db	1139	GCCGTAGCGCTGAGAGCGGGGAGCGACCTCCGGGGTGGCGGTGGGGCGGCTCCGCTG	1198
Qy	901	GCTTACCCCACTCCAGCTCCGGCAGCTCCTCGAGGGGCACTGAGAGGCCGCGCTCACTC	960
Db	1199	GCTTACCCCACTCCAGCTCCGGCAGCTCCTCGAGGGGCACTGAGAGGCCGCGCTCACTC	1258
Qy	961	AAGAGGGGCTCCAAGCCGTGGCGTCTCGGCTCGGTGAGAGAGCCGATGAAGATGGTG	1020
Db	1259	AAGAGGGGCTCCAAGCCGTGGCGTCTCGGCTCGGTGAGAGAGCCGATGAAGATGGTG	1318
Qy	1021	TCCCAGAGCTTACCCAGCGCTTTTGGGCTGTCTCGGACAGGAAAGTGGCCAGTCCGCTG	1080
Db	1319	TCCCAGAGCTTACCCAGCGCTTTTGGGCTGTCTCGGACAGGAAAGTGGCCAGTCCGCTG	1378
Qy	1081	GCGCTCATCGTAGCATCTTTTGGGCTGTGTGGGCCCCCATACAGCTGCTGATGATCATC	1140
Db	1379	GCGCTCATCGTAGCATCTTTTGGGCTGTGTGGGCCCCCATACAGCTGCTGATGATCATC	1438
Qy	1141	CGGGCCGCTGCCATGGCCACTGGTCCCTGACTACTGTGATAGAAAACCTCTCTTGCTG	1200
Db	1439	CGGGCCGCTGCCATGGCCACTGGTCCCTGACTACTGTGATAGAAAACCTCTCTTGCTG	1498
Qy	1201	CTGTGGGCCAACTCGGCTGTCAACCCCTCTCTACCTCTGTGSCCACCACAGCTCCCG	1260
Db	1499	CTGTGGGCCAACTCGGCTGTCAACCCCTCTCTACCTCTGTGSCCACCACAGCTCCCG	1558
Qy	1261	CGGGCCCTTACCAAGCTGCTGTGCCCCGAGAAGCTCAAAATCCAGCCCCACAGCTCCCTG	1320
Db	1559	CGGGCCCTTACCAAGCTGCTGTGCCCCGAGAAGCTCAAAATCCAGCCCCACAGCTCCCTG	1618
Qy	1321	GAGCACTGCTGGAAG 1335	
Db	1619	GAGCACTGCTGGAAG 1633	
RESULT 11			
ID	ADD22860 standard; cDNA; 2699 BP.		
AC	ADD22860;		
XX			
DT	15-JAN-2004 (first entry)		
DE	Human full length cDNA encoding histamine H3 receptor.		
XX			
KW	Human; ss; Histamine H3 receptor; GPCR; G protein-coupled receptor; gene;		
KW	depression; anxiety; schizophrenia; Parkinson's disease; obesity;		
KW	hypertension; Tourette's syndrome; sexual dysfunction; drug addiction;		
KW	drug abuse; cognitive disorder; Alzheimer's disease;		
KW	obsessive-compulsive behaviour; panic attack; pain; eating disorder;		
KW	anorexia; cardiovascular disorder; cerebrovascular disorder; diabetes;		
KW	constipation; arrhythmia; ulcer; asthma; allergy; inflammation;		
XX			
OS	Homo sapiens.		
XX			
FH	Location/Qualifiers		
FT	299..1636		
FT	/*tag= a		
FT	/product= "Histamine H3 receptor"		
XX			
PN	US6437100-B1.		

[illegible]

719	TCATACGGGGCCACGAGGGTGACACGGGGGGGAGTGCGGAAGATGCTCTCGTGTGG	718
481	GTGCTGGCGCTTCTCTGTATACGGACCAAGCCATCTCTGAGCTGGGAGTACTGTCTCGGGGGC	540
779	GTGCTGGCGCTTCTCTGTATACGGACCAAGCCATCTCTGAGCTGGGAGTACTGTCTCGGGGGC	838
541	AGCTCCATCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTACTTCTCATC	600
839	AGCTCCATCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTACTTCTCATC	898
601	ACGGCTTCCACCTTGGAGTCTTTTACGGCCCTTCTCTCAGCGTCACTTCTTTTAACTCAGC	660
899	ACGGCTTCCACCTTGGAGTCTTTTACGGCCCTTCTCTCAGCGTCACTTCTTTTAACTCAGC	958
661	ATCTACTCTGAACATCTCAGAGCGCACCGCGCTCCGGCTGGATGGGGTCTCGAGAGCGAGCC	720
959	ATCTACTCTGAACATCTCAGAGCGCACCGCGCTCCGGCTGGATGGGGTCTCGAGAGCGAGCC	1018
721	GGCCCCGAGCCCTCTCCGAGGCCAGGCCCTACACACCCACCGCTTGGCTGGCTGGGGC	780
1019	GGCCCCGAGCCCTCTCCGAGGCCAGGCCCTACACACCCACCGCTTGGCTGGCTGGGGC	1078
781	TGCTGGCAGAAAGGGGCGACGGGGAGGCCATGCCGCTGCACAGGTATGGGTGGGTAGCGC	840
1079	TGCTGGCAGAAAGGGGCGACGGGGAGGCCATGCCGCTGCACAGGTATGGGTGGGTAGCGC	1138
841	GCCGTAGGCGCTGAGGGCGGGGAGCGCACTCCGGGGGTGGCGGTGGGGGGCGGCTCGCGT	900
1139	GCCGTAGGCGCTGAGGGCGGGGAGCGCACTCCGGGGGTGGCGGTGGGGGGCGGCTCGCGT	1198
901	GCTTCAACCCACTCGAGCTCCGGCAGTCTCTCGAGGGGCACTGAGAGGCCCGCGTCTCACTC	960
1199	GCTTCAACCCACTCGAGCTCCGGCAGTCTCTCGAGGGGCACTGAGAGGCCCGCGTCTCACTC	1258
961	AAGAGGGGCTCCAAGCGTGGCGCTCTCGGCCCTCGCTGGAGAGCGCATGAAGATGGTG	1020
1259	AAGAGGGGCTCCAAGCGTGGCGCTCTCGGCCCTCGCTGGAGAGCGCATGAAGATGGTG	1318
1021	TCCCAGAGCTTCAACCGAGCGCTTTTCGGCTGTCTCGGACAGGAAGTGGCCAGTCCGCTG	1080
1319	TCCCAGAGCTTCAACCGAGCGCTTTTCGGCTGTCTCGGACAGGAAGTGGCCAGTCCGCTG	1378
1081	GCCTCATCTGTAGCATCTTTTGGGCTCTGTGTGGCCCCCATACACGCTGCTGATGATCATC	1140
1379	GCCTCATCTGTAGCATCTTTTGGGCTCTGTGTGGCCCCCATACACGCTGCTGATGATCATC	1438
1141	CGGGCCGCTGCCATGGGCCACTGGTCCCTGACTACTGTGGTACGAAAACCTCTCTTGGGCTC	1200
1439	CGGGCCGCTGCCATGGGCCACTGGTCCCTGACTACTGTGGTACGAAAACCTCTCTTGGGCTC	1498
1201	CTGTGGGCGCAACTCGGCTGTCAACCCCTGTCTCTACCTCTGTGCCACACAGCTTCGCGC	1260
1499	CTGTGGGCGCAACTCGGCTGTCAACCCCTGTCTCTACCTCTGTGCCACACAGCTTCGCGC	1558
1261	CGGGCTTTCACAAAGTGTCTGTGCCCCCGAAGCTCAAAATCCAGCCCCACAGCTCCCTG	1320
1559	CGGGCTTTCACAAAGTGTCTGTGCCCCCGAAGCTCAAAATCCAGCCCCACAGCTCCCTG	1618
1321	GAGCACTGCTGGAG	1335
1619	GAGCACTGCTGGAAG	1633

RESULT 12

ADQ89179
ID ADQ89179 standard; cDNA: 2699 BP.

XX
XX

AC ADQ89179;

XX

DT 21-OCT-2004 (first entry)
YY

XX DE

urological disorder; uropathic; cytostatic; urinary incontinence;
benign prostatic hyperplasia; human; Gene; ss.

Homo sapiens.

Key
CDS
Location/Qualifiers
299..1636
/*tag= a
/product= "urological disorder related protein 8203"

WO2004065576-A2.

05-AUG-2004.

14-JAN-2004: 2004WO-US000750.

15-JAN-2003: 2003US-0440318P.

04-FEB-2003; 2003US-0444783P.

27-MAR-2003; 2003US-0457901P.

08-MAY-2003; 2003US-0468775P.

19-MAY-2003; 2003US-0471614P.
16-JUN-2003; 2003US-0478742D

16-JUN-2003; 2003US-04/8742P.
18-JUL-2003; 2003US-0488529P.

18-JUL-2003; 2003US-0488329F;
30-JUL-2003; 2003US-0491156P;

02-SEP-2003; 2003US-0499594P.

26-SEP-2003; 2003US-0506332P.

החלטת הוועדה להקמת מוזיאון תולדות העיר תל אביב

(MILL-) MILLENNIUM PHARM INC.

Karicheti V, Silos-Santiago I, Eliasot SD,

WPI; 2004-562167/54.
B-BENB. AD000100

P-FSDB; ADQ89180.

211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological disorder.

Claim 1; SEQ ID NO 131; 542pp; English.

The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) a method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological disorder; and (3) a method for treating a subject having a urological disorder. The compound has uropathic and cytostatic activities. The polypeptides related to urological disorders are useful for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Disorders include urinary incontinence and benign prostatic hyperplasia. The present sequence encodes a human urological disorder related protein, which is used in the exemplification of the present invention.

Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;

Query Match 100.0%; Score 1335; DB 13; Length 2699;
Best Local Similarity 100.0%; Pred. No. 3.3e-217;
Matches 1335; Conservative 0; Mismatches 0; Indels 0;

Qy 1 ATGGAGCGCGCGCCGCCGACGGGCGCTGAACGCTTCGGGGCGCTGGCGGGCGATGCG 60

[illegible]

Db 299 ATGGAGCGCGCGCGCGCCCGACGGCGCGCTGAACGCTTCGGGGCGCGCTGGCGGGCGATCGG 358

[illegible]

01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Db 359 GCGGCGGGCGGGCGGGCTTCTCGGCAGCCTGGACCGCGGTGCTGGCCGGCTC 418

Ds	419	ATGGCGCTCTCATCGTGGCCACCGTGTGGGCAACGGGCTGGTATGCTCGCCTTCGTG	478
Qy	181	GCCGACTCGAGCTCCGACACAGAACAACTTCCTCTGCTCAACTCGCCATCTCCGAC	240
Ds	479	GCCGACTCGAGCTCCGACACAGAACAACTTCCTCTGCTCAACTCGCCATCTCCGAC	538
Qy	241	TTCTCTCGTGGGCGCTCTTGATCCCATCTGATGATGATGATGATGATGATGATGATG	300
Ds	539	TTCTCTCGTGGGCGCTCTTGATCCCATCTGATGATGATGATGATGATGATGATGATG	598
Qy	301	ACCTTCGGCGGGGCTCTGCAAGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTG	360
Ds	599	ACCTTCGGCGGGGCTCTGCAAGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTG	658
Qy	361	TCTGCTTCACATGCTGCTCATGCTACGCTACGACCGCTTCCTGTCGGTACCCGAGGCTC	420
Ds	659	TCTGCTTCACATGCTGCTCATGCTACGCTACGACCGCTTCCTGTCGGTACCCGAGGCTC	718
Qy	421	TCATACCGGGCCAGCAGGGTGACACGGCGGGGAGTGCGGAAGATGCTGTGTGGTGG	480
Ds	719	TCATACCGGGCCAGCAGGGTGACACGGCGGGGAGTGCGGAAGATGCTGTGTGGTGG	778
Qy	481	GTGCTGGCTTCTCTGTATGACGACAGCCATCTCTGAGCTGGGAGTACTGTCCGGGGC	540
Ds	779	GTGCTGGCTTCTCTGTATGACGACAGCCATCTCTGAGCTGGGAGTACTGTCCGGGGC	838
Qy	541	AGCTTCATCCCGAGGGCCACTGCTATGCCGAGTCTTCTTACAACTGGTACTTCTCTATC	600
Ds	839	AGCTTCATCCCGAGGGCCACTGCTATGCCGAGTCTTCTTACAACTGGTACTTCTCTATC	898
Qy	601	ACGGCTTCACACCTCGAGTCTTCTTACGCTTCTCTCAGCGTCACTTCTTTAACTCAGC	660
Ds	899	ACGGCTTCACACCTCGAGTCTTCTTACGCTTCTCTCAGCGTCACTTCTTTAACTCAGC	958
Qy	661	ATCTACCTGAACATCCAGAGGCGCAACCGCTCTCCGGCTGGATGGGCTCGAGAGCAGCC	720
Ds	959	ATCTACCTGAACATCCAGAGGCGCAACCGCTCTCCGGCTGGATGGGCTCGAGAGCAGCC	1018
Qy	721	GGCCCGAGCCCTCCGAGGCGCCAGCCCTCACACCCCAACCGCTGGCTGGCTGGGGC	780
Ds	1019	GGCCCGAGCCCTCCGAGGCGCCAGCCCTCACACCCCAACCGCTGGCTGGCTGGGGC	1078
Qy	781	TGCTGGCAGAGGGGCACGGGAGGCGCATGCGCTGACAGGTATGGGGTGGGTGAGGGC	840
Ds	1079	TGCTGGCAGAGGGGCACGGGAGGCGCATGCGCTGACAGGTATGGGGTGGGTGAGGGC	1138
Qy	841	GCCGTAGGCGCTGAGCCGGGAGGCGACCTTCGGGGTGGCGGTGGGGCGGCTCCGCTG	900
Ds	1139	GCCGTAGGCGCTGAGCCGGGAGGCGACCTTCGGGGTGGCGGTGGGGCGGCTCCGCTG	1198
Qy	901	GCTTACCCACCTCAGCTCCGGCAGCTCTCGAGGGGCACTGAGAGGCGCGCTCACTC	960
Ds	1199	GCTTACCCACCTCAGCTCCGGCAGCTCTCGAGGGGCACTGAGAGGCGCGCTCACTC	1258
Qy	961	AAGAGGGCTCAAGCGCTGGCGCTCTCGGCTCGCTGAGAGCGCATGAAGATGGT	1020
Ds	1259	AAGAGGGCTCAAGCGCTGGCGCTCTCGGCTCGCTGAGAGCGCATGAAGATGGT	1318
Qy	1021	TCCGAGAGTTTCAACAGCGCTTTTGGGTGTCTCGGAGCAGGAAAGTGCCCAAGTCGCTG	1080
Ds	1319	TCCGAGAGTTTCAACAGCGCTTTTGGGTGTCTCGGAGCAGGAAAGTGCCCAAGTCGCTG	1378
Qy	1081	GCGCTATGCTAGCATCTTTGGGTCTGCTGGGCGCCATACAGCTGCTGATGATCATC	1140
Ds	1379	GCGCTATGCTAGCATCTTTTGGGTCTGCTGGGCGCCATACAGCTGCTGATGATCATC	1438
Qy	1141	CGGGCGCTGCTGATGGCCACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200
Ds	1439	CGGGCGCTGCTGATGGCCACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1498
Qy	1201	CTGTGGGCAACTCGGCTGTGCAACCTGTCTTACTTACTTACTTACTTACTTACTTACTT	1260
Ds	1499	CTGTGGGCAACTCGGCTGTGCAACCTGTCTTACTTACTTACTTACTTACTTACTTACTT	1558
Qy	1261	CGGGCTTCCACCAAGCTCTGTGCCCCCAGAGCTCAAAATCCAGCCACAGCTCCCTG	1320
Ds	1559	CGGGCTTCCACCAAGCTCTGTGCCCCCAGAGCTCAAAATCCAGCCACAGCTCCCTG	1618
Qy	1321	GAGCACTGCTGGAAG 1335	
Ds	1619	GAGCACTGCTGGAAG 1633	
RESULT 13			
ADR31456			
ID	ADR31456	standard; cDNA; 2699 BP.	
XX	AC	ADR31456;	
XX	XX	04-NOV-2004 (first entry)	
DE	XX	Human histamine H3 receptor cDNA #1.	
KW	XX	Human; Parkinson's disease; obesity; Alzheimer's disease; pain; stress;	
KW	XX	ulcer; constipation; non-insulin dependent diabetes mellitus; gene; ss;	
KW	XX	histamine H3 receptor.	
OS	XX	Homo sapiens.	
FX	XX	Key	Location/Qualifiers
FT	XX	CDS	299..1636
FT	XX	/*tag= a	/product= "Human histamine H3 receptor protein"
XX	XX	US2004156845-A1.	
PN	XX	12-AUG-2004.	
PD	XX	02-DEC-2003; 2003US-00727021.	
PF	XX	07-OCT-1998; 98US-00167354.	
PR	XX	21-AUG-2000; 2000US-00642852.	
PA	XX	(LOVE/) LOVENBERG T W.	
PA	XX	(ERLA/) ERLANDER M.	
PA	XX	(HUVA/) HUVAR A.	
PA	XX	(PYAT/) PYATI J.	
PI	XX	Lovenberg TW, Erlander M, Huvar A, Pyati J;	
XX	XX	WPI; 2004-592726/57.	
DR	XX	P-PSDB; ADR31458.	
XX	XX	Novel isolated and purified human histamine H3 receptor protein useful	
PT	XX	for identifying modulators utilized for treating Parkinson's disease,	
PT	XX	obesity, Alzheimer's disease, pain, stress or ulcers.	
PS	XX	Claim 2; SEQ ID NO 5; 26pp; English.	
CC	XX	The present invention provides a human histamine H3 receptor protein and	
CC	XX	nucleic acid encoding such protein. The invention is useful for	
CC	XX	identifying compounds that modulate the activity of human histamine H3	
CC	XX	receptor. The invention is useful for treating a condition that is	
CC	XX	mediated by a human histamine H3 receptor in a patient and for treating	
CC	XX	Parkinson's disease, obesity, Alzheimer's disease, pain, stress, ulcers,	
CC	XX	constipation and non-insulin dependent diabetes mellitus. The present	
CC	XX	sequence is a human histamine H3 receptor cDNA.	
SQ	XX	Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;	
Query Match			
Best Local Similarity 100.0%; Score 1335; DB 13; Length 2699;			
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	ATGGAGCGCGCCCGCCGAGCGGCGCTGAAACGCTTCGGGGCGCTGCGGGCGATGCG	60

of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridize to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia), disorders of the adrenal gland, disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR-encoding nucleic acid of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1338 BP; 193 A; 476 C; 418 G; 251 T; 0 U; 0 Other;

Query Match 99.9%; Score 1333.4; DB 12; Length 1338;
Best Local Similarity 99.9%; Pred. No. 6.1e-217;
Matches 1334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGCGCGCGCCCGACGCGGCGCTTGAACGCTTCGGGGCGCTGCGGGCGATGCG 60
DB 1 ATGAGCGCGCGCCCGACGCGGCGCTTGAACGCTTCGGGGCGCTGCGGGCGATGCG 60

QY 61 GCGGCGGCGGCGGCGCGCGCTTCTCGGAGCTTGAACGCGGCTGCGGGCGATGCG 120
DB 61 GCGGCGGCGGCGGCGCGCGCTTCTCGGAGCTTGAACGCGGCTGCGGGCGATGCG 120

QY 121 ATGCGCTGCTCATCTGCGGCGAGCTTCTGCGGAGCTTGAACGCGGCTGCGGGCGATGCG 180
DB 121 ATGCGCTGCTCATCTGCGGCGAGCTTCTGCGGAGCTTGAACGCGGCTGCGGGCGATGCG 180

QY 181 GCCGACTCGAGCTCGGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGAC 240
DB 181 GCCGACTCGAGCTCGGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGAC 240

QY 241 TTCCTCGTGGCGCTTCTGCAATCCCACTGTATGACCTACGCTGACAGCGCGCTGG 300
DB 241 TTCCTCGTGGCGCTTCTGCAATCCCACTGTATGACCTACGCTGACAGCGCGCTGG 300

QY 301 ACCTTCGCGCGGCGCTTCTGCAATCCCACTGTATGACCTACGCTGACAGCGCGCTGG 360
DB 301 ACCTTCGCGCGGCGCTTCTGCAATCCCACTGTATGACCTACGCTGACAGCGCGCTGG 360

QY 361 TCTGCTTCAACATCTGCTCATAGCTACGACCGCTTCTTCTGCTCAACCTCGCCATCTCCGAC 420
DB 361 TCTGCTTCAACATCTGCTCATAGCTACGACCGCTTCTTCTGCTCAACCTCGCCATCTCCGAC 420

QY 421 TCATACCGGCGCCAGAGGTTGACACGCGGCGGAGTGGGAGATGCTGCTGTGGTGG 480
DB 421 TCATACCGGCGCCAGAGGTTGACACGCGGCGGAGTGGGAGATGCTGCTGTGGTGG 480

QY 481 GTGCTGGCTTCTGCTGTACGACCGACCTTCCTGAGCTGGAGTACCTGCTCCGGGGG 540
DB 481 GTGCTGGCTTCTGCTGTACGACCGACCTTCCTGAGCTGGAGTACCTGCTCCGGGGG 540

QY 541 AGCTCCATCCCGAGGCGACCTGCTATGCCGAGTTCTTCTACAACTGGTACTTCTCTCATC 600

DB 541 AGCTCCATCCCGAGGCGACCTGCTATGTCGAGTTCTTCTACAACTGGTACTTCTCTCATC 600
QY 601 ACGGCTTCCACCTCGAGATTCTTTACGCGCTTCTTACGCGTCACTTCTTTAACTCAGC 660
DB 601 ACGGCTTCCACCTCGAGATTCTTTACGCGCTTCTTACGCGTCACTTCTTTAACTCAGC 660
QY 661 ATCTACCTGAACATCCAGAGCGGACCGGCTTCCGCTGGATGGGCTCGAGAGCGAGCC 720
DB 661 ATCTACCTGAACATCCAGAGCGGACCGGCTTCCGCTGGATGGGCTCGAGAGCGAGCC 720
QY 721 GGGCCCGAGCGCTTCCGAGGCGGACCGCTTCCAGCCCGACCGCTTGGTGTGGGGC 780
DB 721 GGGCCCGAGCGCTTCCGAGGCGGACCGCTTCCAGCCCGACCGCTTGGTGTGGGGC 780
QY 781 TGCTGGAGAGAGGCGACCGGAGGCGCATGCGCTGCAAGTATGGGGTGGGTGAGGGC 840
DB 781 TGCTGGAGAGAGGCGACCGGAGGCGCATGCGCTGCAAGTATGGGGTGGGTGAGGGC 840
QY 841 GCCGTAGGCGCTGAGGCGGCGGAGCGGACCTTCCGCGGCTGCGGGCTGGGGCGGCTCCGTCG 900
DB 841 GCCGTAGGCGCTGAGGCGGCGGAGCGGACCTTCCGCGGCTGCGGGCTGGGGCGGCTCCGTCG 900
QY 901 GCTTCAACCTCAGCTCCGAGCTCCGAGGCGGACCTTCCGAGGCGGCTGAGAGCGCGCTCACTC 960
DB 901 GCTTCAACCTCAGCTCCGAGCTCCGAGGCGGACCTTCCGAGGCGGCTGAGAGCGCGCTCACTC 960
QY 961 AAGAGGGCTCAAGCGCTGCGGCTTCCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1020
DB 961 AAGAGGGCTTCAAGCGCTGCGGCTTCCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1020
QY 1021 TCCAGAGCTTCAAGCGCTTCCGCGCTTCCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1080
DB 1021 TCCAGAGCTTCAAGCGCTTCCGCGCTTCCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1080
QY 1081 GCCGTATGCTGAGCATCTTTGGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTG 1140
DB 1081 GCCGTATGCTGAGCATCTTTGGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTG 1140
QY 1141 CGGCGCGCTGCGATGGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1200
DB 1141 CGGCGCGCTGCGATGGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1200
QY 1201 CTGTGGGCGAACTGGGCTGCAACCTGCTTCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 1201 CTGTGGGCGAACTGGGCTGCAACCTGCTTCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1261 CGGCGCTTCAACCAAGCTGCTTCCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1320
DB 1261 CGGCGCTTCAACCAAGCTGCTTCCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1320
QY 1321 GAGCACTGCTGAG 1335
DB 1321 GAGCACTGCTGAG 1335

RESULT 15
AA84572
ID AA84572 standard; DNA; 2050 BP.
XX
AC AA84572;
XX
DT 14-SEP-1999 (first entry)
XX
DE Human G-protein conjugate-type receptor protein coding sequence.
KW Guanosine triphosphate binding protein; signal transduction regulation;
KW G-protein conjugate-type receptor protein; learning difficulty; BG2;
KW muscarinic acetylcholine receptor; physiological function disorder;
KW blood pressure; digestion; sleep; therapy; human; ss.
OS Homo sapiens.
XX
PN W09933978-A1.

XX 08-JUL-1999.
PD XX
PF 25-DEC-1998; 98WO-JP005967.
XX
PR 26-DEC-1997; 97JP-00361187.
XX
PA (BANY) BANYU PHARM CO LTD.
XX
PI Itadani H, Takimura T, Nakamura T, Ohta M;
XX
DR WPI; 1999-419107/35.
DR P-PSDB; AY22208.
XX
PT GTP binding protein conjugate-type receptor protein for screening
PT candidate drugs for signal transduction modification.
XX
PS Claim 2; Page 67-72; 77pp; English.
XX
CC This sequence encodes the human guanosine triphosphate binding protein (G
CC -protein) conjugate-type receptor protein (designated BG2) of the
CC invention. BG2 is a member of the G-protein conjugate-type receptor super
CC family and shows significant homology to other muscarinic acetylcholine
CC receptors. BG2 can be used in a screening method for identifying ligands
CC binding to the BG2 receptor and for compounds which are agonists or
CC antagonists to the binding of ligands to BG2 receptor, and which can be
CC used for the regulation of signal transduction, and thus for the
CC prevention and treatment of memory and learning difficulties and
CC disorders of the control of physiological functions such as blood
CC pressure, digestion and sleep
XX
SQ Sequence 2050 BP; 310 A; 682 C; 650 G; 408 T; 0 U; 0 Other;

Query Match 99.8%; Score 1332.4; DB 2; Length 2050;
Best Local Similarity 99.9%; Pred. No. 9.1e-217;
Matches 1333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAGCGGCGCCCGGACGGGCGGCTGAAACGCTTCGGGGCGCGTGGGGCGGATGCG 60
DB |||||||
271 ATGAGAGCGGCGCGCGCGGCGGCTGAAACGCTTCGGGGCGCGTGGGGCGGAGGG 330
QY 61 GCGGGCGGCGGCGGCGGCGGCTTCGCGAGCGCTGGAACGCGCGGCTGCGCGGCTC 120
DB |||||||
331 GCGGGCGGCGGCGGCGGCGGCTTCGCGAGCGCTGGAACGCGCGGCTGCGCGGCTC 390
QY 121 ATGGCGCTGCTCATCGTGGCCACGCTGCTGGCAACGCGCTGCTATGCTGCGCTTCGTG 180
DB |||||||
391 ATGGCGCTGCTCATCGTGGCCACGCTGCTGGCAACGCGCTGCTATGCTGCGCTTCGTG 450
QY 181 GCCGACTCGAGCTCCGCAACCGAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGAC 240
DB |||||||
451 GCCGACTCGAGCTCCGCAACCGAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGAC 510
QY 241 TTCCTGCTGGCGCTTCGCAATCCCACTGATGATACCTACGCTGACAGCGCGCTGG 300
DB |||||||
511 TTCCTGCTGGCGCTTCGCAATCCCACTGATGATACCTACGCTGACAGCGCGCTGG 570
QY 301 ACCTTCGGCGGGGCGCTTCGCAAGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
DB |||||||
571 ACCTTCGGCGGGGCGCTTCGCAAGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 630
QY 361 TCTGCTTCAACATCGTCTCATAGTACGACCGCTTCTGCTGGTCAACCGGAGCGGTG 420
DB |||||||
631 TCTGCTTCAACATCGTCTCATAGTACGACCGCTTCTGCTGGTCAACCGGAGCGGTG 690
QY 421 TCATACCGGGGCCAGCAGGGTGACACGCGGGGGGAGTGCAGGAATGCTGCTGGTGG 480
DB |||||||
691 TCATACCGGGGCCAGCAGGGTGACACGCGGGGGGAGTGCAGGAATGCTGCTGGTGG 750
QY 481 GTGCTGGCTTCCTGCTGTACGGACAGGCATCTGAGCTGGGAGTACCTGTCGGGGGG 540
DB |||||||
751 GTGCTGGCTTCCTGCTGTACGGACAGGCATCTGAGCTGGGAGTACCTGTCGGGGGG 810

QY 541 AGCTCCATCCCGAGGGCCACTGCTATATGCGAGTTCTTCTTAACTGGTACTTCTCTCATC 600
DB |||||||
811 AGCTCCATCCCGAGGGCCACTGCTATATGCGAGTTCTTCTTAACTGGTACTTCTCTCATC 870
QY 601 ACGGCTTCCACCCCTGGAGTTCCTTACGCGCTTCCCTCAGCGTCACTTCTTTAACTCAGC 660
DB |||||||
871 ACGGCTTCCACCCCTGGAGTTCCTTACGCGCTTCCCTCAGCGTCACTTCTTTAACTCAGC 930
QY 661 ATCTACCTGAACATCCAGAGGCGCACCGCGCTTCCGCTGGATGGGCTCGAGAGGCGCC 720
DB |||||||
931 ATCTACCTGAACATCCAGAGGCGCACCGCGCTTCCGCTGGATGGGCTCGAGAGGCGCC 990
QY 721 GGGCCGAGCGCCCTTCCGAGGCGCGAGCGCTCAACACCCCGACCGCTGCTGGGGC 780
DB |||||||
991 GGGCCGAGCGCCCTTCCGAGGCGCGAGCGCTCAACACCCCGACCGCTGCTGGGGC 1050
QY 781 TGCTGGCAGAGAGGGGACGCGGGAGGCGCATGCGCTGACAGGTATGGGGTGGGTGAGGGC 840
DB |||||||
1051 TGCTGGCAGAGAGGGGACGCGGGAGGCGCATGCGCTGACAGGTATGGGGTGGGTGAGGGC 1110
QY 841 GCCGTAGGCGCTGAGGGCGGGAGGCGCACCTTCGGGGGTGGCGGTGGGGCGGCTCCGCTG 900
DB |||||||
1111 GCCGTAGGCGCTGAGGGCGGGAGGCGCACCTTCGGGGGTGGCGGTGGGGCGGCTCCGCTG 1170
QY 901 GCTTACCCACTCCAGCTCCGCGAGCTTCGAGGGGCACTGAGAGGCGCGCTCACTC 960
DB |||||||
1171 GCTTACCCACTCCAGCTCCGCGAGCTTCGAGGGGCACTGAGAGGCGCGCTCACTC 1230
QY 961 AAGAGGGGCTCAAGCGCTCGGCGCTTCGCGCTCGCTGGAGAGGCGCATGAAGATGGTG 1020
DB |||||||
1231 AAGAGGGGCTCAAGCGCTCGGCGCTTCGCGCTCGCTGGAGAGGCGCATGAAGATGGTG 1290
QY 1021 TCCAGAGCTTCAACCCAGCGCTTTCGGCTGTCTCGGACAGGAAAGTGGCCAAAGTCGCTG 1080
DB |||||||
1291 TCCAGAGCTTCAACCCAGCGCTTTCGGCTGTCTCGGACAGGAAAGTGGCCAAAGTCGCTG 1350
QY 1081 GCCGTATCGTGAAGCATCTTTGGGCTCTGCTGGGCGCCCATACAACGCTGCTGATGATCATC 1140
DB |||||||
1351 GCCGTATCGTGAAGCATCTTTGGGCTCTGCTGGGCGCCCATACAACGCTGCTGATGATCATC 1410
QY 1141 CGGGCGGCTTGCATGGGCACTGGCTCCCTGACTACTGTTAGGAAACCTCTTCTGGGCTC 1200
DB |||||||
1411 CGGGCGGCTTGCATGGGCACTGGCTCCCTGACTACTGTTAGGAAACCTCTTCTGGGCTC 1470
QY 1201 CTGTGGGCGCAACTCGGCTGTCAACCGCTGTCTTACCTCTGTGCGCACCAAGCTTCCGC 1260
DB |||||||
1471 CTGTGGGCGCAACTCGGCTGTCAACCGCTGTCTTACCTCTGTGCGCACCAAGCTTCCGC 1530
QY 1261 CGGGCTTTCACCAAGCTCTCTGCGCCCGAGAGCTCAAAATCCAGCCCGACAGCTCCCTG 1320
DB |||||||
1531 CGGGCTTTCACCAAGCTCTCTGCGCCCGAGAGCTCAAAATCCAGCCCGACAGCTCCCTG 1590
QY 1321 GAGCACTGCTGAA 1334
DB |||||||
1591 GAGCACTGCTGAA 1604

Search completed: June 2, 2005, 06:01:47
Job time : 715.507 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 05:10:00 ; Search time 4400.8 Seconds
(without alignments)
11546.944 Million cell updates/sec

Title: US-10-727-021-6

Perfect score: 1335

Sequence: 1 atggagcgccgcgcgcga.....ccctggagcactgctggaag 1335

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	677	50.7	732	7	CF147822	AGENCOURT
2	541.8	40.6	890	4	BI731453	603354331
3	516	38.7	716	7	CN423054	170004245
4	462.8	34.7	672	6	CB556920	AMGNNUC:U
5	412.6	30.9	910	2	BE783826	601471053
6	390.8	29.3	547	6	CB611519	AMGNNUC:N
7	385.4	28.9	1103	4	BM548665	AGENCOURT
8	371.2	27.8	499	2	BF567596	UT-R-B00-
9	369.6	27.7	519	2	AW669811	113386 MA
10	340.8	25.5	1046	5	BQ950659	AGENCOURT
11	331	24.8	946	5	BQ668856	AGENCOURT
12	294.4	22.1	842	7	CO403631	AGENCOURT
13	277	20.7	653	6	BY727560	BY727560
14	272.8	20.4	434	6	CB758850	AMGNNUC-S
15	264.2	19.8	853	6	CD326085	AGENCOURT
16	240.6	18.0	490	6	CB725716	AMGNNUC:U
17	224.2	16.8	643	1	AL848045	AL848045
18	218	16.3	533	6	CB154982	K-EST0213
19	214.4	16.1	258	2	AW654609	104607 MA
20	212	15.9	484	1	AA859887	UT-R-E0-C
21	208	15.6	538	2	AW654493	103977 MA
22	197.8	14.8	975	9	CNS039RV	Tetraodon
23	189.8	14.2	236	2	BE063702	QV3-BT029
24	180.8	13.5	281	2	BB592940	BB592940

ALIGNMENTS

RESULT 1
CF147822
LOCUS CF147822 732 bp mRNA linear EST 25-JUL-2003
DEFINITION AGENCOURT_14740187 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:6971899 5', mRNA sequence.
ACCESSION CF147822
VERSION CF147822.1 GI:33244090
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 732)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: IRB102 row: b column: 06
High quality sequence stop: 610.

FEATURES

Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971899"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_lib="NIH_MGC_145"
/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XbaI-XhoI-3',
5'-EcoRV-XbaI/NotI-3', EcoRV (if a cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRB1.presv.dat

CC580463 CH240_375
AY404934 Homo sapi
BU147486 AGENCOURT
AY404935 Pan trogl
BM805220 AGENCOURT
AL536991 AL536991
BM548382 AGENCOURT
CB565879 AGENCOURT
BI064672 pgfln.pk0
BC035047 Homo sapi
CD804122 UT-M-GV0-
AK081248 Mus muscu
CV026860 4931 Full
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BM907142 AGENCOURT
BX355053 BX355053
CR366545 CR366545
AW327105 2622 MAR
AL178693 Tetraodon
BX424634 BX424634
CK958826 409592 B

25 174.4 13.1 775 9 CC580463
26 173.6 13.0 1440 9 AY404934
27 173.4 13.0 916 5 BU147486
28 172.4 12.9 1440 9 AY404935
29 172.2 12.9 1048 4 BM805220
30 171.6 12.9 975 1 AL536991
31 171.6 12.9 1078 4 BM548382
32 169.8 12.7 855 6 CB565879
33 167.6 12.6 650 4 BI064672
34 166.4 12.5 2410 3 BC035047
35 165.8 12.4 795 6 CD804122
36 165.2 12.4 3816 3 AK081248
37 164.2 12.3 623 7 CV026860
38 164.2 12.3 812 1 AL537084
39 164.2 12.3 1108 5 BM907142
40 162 12.1 952 5 BX355053
41 161.8 12.1 727 7 CR366545
42 161.2 12.1 206 2 AW327105
43 160.2 12.0 1037 9 CNS022VG
44 159.4 11.9 887 5 BX424634
45 159.2 11.9 732 7 CK958826


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QY 1251 CAGCTTCGCGCGGCTTCCAAAGCTGCTGTGCCCCCAAGAGCTCAAAATCCAGCCCCA 1310
Db 657 CAGCTTCGCTAGAGCCTTCCAAAGCTCTCTGTGCCCCCAAGAGCTCAAGGTCCAGCCCCA 716
QY 1311 CAGCTCCCTGGAGCACTGCTGAAG 1335
Db 717 TGGCTCCCTGGAGCACTGCTGAAG 741

RESULT 3
CN423054 716 bp mRNA linear EST 16-MAY-2004
LOCUS 1700424504731 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN423054
ACCESSION CN423054
VERSION CN423054.1 GI:47410648
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 716)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Pang, R., Quesler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
JOURNAL Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
COMMENT Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 716 Std Error: 0.00.
FEATURES
source
1..716
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
/clone_lib="GRN ES"
/note="oligo dt primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN
Query Match 38.7%; Score 516; DB 7; Length 716;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 GCGCGCTTCTGCATCCCACTGATGACCTTACCTAGTGTGACAGGCGGTGGACCTTCGCG 309
Db 201 GCGCGCTTCTGCATCCCACTGATGATGACCTTACCTAGTGTGACAGGCGGTGGACCTTCGCG 260
QY 310 CGGGGCGCTTGCAGCTGTGGCTGTAGTGGACTACTGCTGTGTGACCTCTCTGCTTC 369
Db 261 CGGGGCGCTTGCAGCTGTGGCTGTAGTGGACTACTGCTGTGTGACCTCTCTGCTTC 320
QY 370 AACATCTGTGCTCATCAGCTTACGACCGCTTCTCTGTGTCACCGCGGTCTCATACCGG 429
Db 321 AACATCTGTGCTCATCAGCTTACGACCGCTTCTCTGTGTCACCGCGGTCTCATACCGG 380
QY 430 GCCAGCAGGGGTGACACGCGCGGGGACGTCGCGAAGATGCTGCTGTGGGTGTGCGCC 489
Db 381 GCCAGCAGGGGTGACACGCGCGGGGACGTCGCGAAGATGCTGCTGTGGGTGTGCGCC 440
QY 490 TTCCTGCTGTACGACACCGACCTCTGAGCTGGGATACCTTCTCGGGGGAGCTCCATC 549
Db 441 TTCCTGCTGTACGACACCGACCTCTGAGCTGGGATACCTTCTCGGGGGAGCTCCATC 500
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QY 550 CCCGAGGGCCACTGTATGCGAGTTCTTCTAACAATGCTACTTCTCTCATCAAGGCTTCC 609
Db 501 CCCGAGGGCCACTGTATGCGAGTTCTTCTAACAATGCTACTTCTCTCATCAAGGCTTCC 560
QY 610 ACCCTGGAGTTCTTTACAGCCCTTCTCAGCGTCACTTCTTTAACTCAGCATCTACCTG 669
Db 561 ACCCTGGAGTTCTTTACAGCCCTTCTCAGCGTCACTTCTTTAACTCAGCATCTACCTG 620
QY 670 AACATCCAGAGGCGCACCGCCTCCGGGTGGATGGGCTTCGAGAGGACGCCGCCCGGAG 729
Db 621 AACATCCAGAGGCGCACCGCCTCCGGGTGGATGGGCTTCGAGAGGACGCCGCCCGGAG 680
QY 730 CCCCTCCCGAGGCCAGCCCTTCACACCCCCACCG 765
Db 681 CCCCTCCCGAGGCCAGCCCTTCACACCCCCACCG 716

RESULT 4
CB556920 672 bp mRNA linear EST 02-APR-2003
LOCUS AMGNNUC:URGP1-00001-D6-A urgp1 (14349) Rattus norvegicus cDNA clone
DEFINITION urgp1-00001-d6 5', mRNA sequence.
ACCESSION CB556920
VERSION CB556920.1 GI:29496320
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 672)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00001 row: d column: 6.
FEATURES
source
1..672
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="urgp1-00001-d6"
/clone_lib="urgp1 (14349)"
/note="Vector: pSPORT1; Rat GPCR library rearranged internal pSPORT vector"

ORIGIN
Query Match 34.7%; Score 462.8; DB 6; Length 672;
Best Local Similarity 89.7%; Pred. No. 4.2e-82;
Matches 497; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 ATGAGAGCGCGCGCCCGGACGCGCGCTTGAAACGCTTCGGGGCGGTGGCGGCGATGCG 60
Db 119 ATGAGAGCGCGCGCCCGGACGCGCGCTTGATGAACGCTTCGGGCGACCTTGCCCGAGAGCG 178
QY 61 GCGGCGCGCGCGCGCGCGCGCTTCTCGGAGCGCTTGACCGGGTGTGCGCGCGCTC 120
Db 179 GCGGCTGAGCGCGCGCGCGCGCTTCTCGGCTGCTGACCGCTGTCTGCTGCGCTC 238
QY 121 ATGGCGCTGCTCATCGTGGCCACGCTGTGGGCAACGCGCTGATGCTCGCTTCGCTG 180
Db 239 ATGGCGCTGCTCATCGTGGCCACGCTGTGGGCAACGCGCTGATGCTCGCTTCGCTG 298
QY 181 GCCGACTCGAGCTCCGCAACCGAGAACAACTTCTTCTGCTCAACCTGCCATCTCCGAC 240
Db 299 GCGATTGAGCTCCGCAACCGAGAACAACTTCTTCTGCTCAACCTGCCATCTCCGAC 358
QY 241 TTCCTGCTGCGCGCTTCTGATCCCACTGTATGATCCCTAGCTGTGACGCGCGCTGG 300
Db 359 TTCCTGCTGCGCGCTTCTGATCCCACTGTATGATCCCTAGCTGTGACGCGCGCTGG 418
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QY 301 ACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGGACTACTGCTGTGCACTCC 360
Db 419 ACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGGACTACTGCTGTGCTCC 478
QY 361 TCTGCTTCAACATCGTGTCTATCATAGCTACGACCGCTTCTGTGCGGTCAACCGAGGGTGC 420
Db 479 TCGGTCTTCAACATCGTGTCTATCATAGCTATGACCGATTCCTGTCACTCACTCGAGCTGTC 538
QY 421 TCATACCGGGCCAGCAGGGTACAGCGGCGGGGACAGTCGCGAAGATGCTGTGTGTGG 480
Db 539 TCTACAGGGCCAGCAGGGGACACGACAGACGGGCGGTTTCGAAGATGGCACTGGTGTGG 598
QY 481 GTGCTGGCTTCTGCTGTACGACGACGACCATCTCTGAGCTGGAGTACTGTCCGGGGC 540
Db 599 GTGCTGGCTTCTGCTGTATGGGCTGCCATCTGAGTTGGAGTACCTGTCTGGTGGC 658
QY 541 AGCTCCATCCCGA 554
Db 659 AGTTCCATCCCGA 672

RESULT 5
LOCUS BE783826 601471053F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874260 5',
DEFINITION mRNA sequence.
ACCESSION BE783826
VERSION BE783826.1 GI:10205024
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9631 row: i column: 13
High quality sequence stop: 601.
FEATURES
source
1..910
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3874260"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 30.9%; Score 412.6; DB 2; Length 910;
Best Local Similarity 96.9%; Pred. No. 4.6e-72;
Matches 443; Conservative 0; Mismatches 9; Indels 5; Gaps 2;
QY 879 TGGCGGTGGGGCGGCTCGTGGCTTCACCACTCCAGCTCCGGCAGCTCCTCGAGGG 938
Db 1 TGGCGGTGGGGCGGCTCGTGGCTTCACCACTCCAGCTCCGGCAGCTCCTCGAGGG 60
QY 939 CACTGAGAGGCGCGCTCACTCAAGAGGGGCTCCAAGCGGTCTCGGCGTCTCGGCTCGCT 998

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Db 61 CACTGAGAGGCGCGCTCACTCAAGAGGCGCTCCAAGCGCTCGGCGTCTCGGCTCGCT 120
QY 999 GGAGAAGCGCATGAAGATGGTGTCCCAAGCTTCAACAGCGCTTTCGGCTGTCTCGGA 1058
Db 121 GGAGAAGCGCATGAAGATGGTGTCCCAAGCTTCAACAGCGCTTTCGGCTGTCTCGGA 180
QY 1059 CAGGAAGTGGCCAGTGGCTGGCGCTCATGTGAGCATCTTTGGGCTCTGTGGGCCCC 1118
Db 181 CAGGAAGTGGCCAGTGGCGCTCATGTGAGCATCTTTGGGCTCTGTGGGCCCC 240
QY 1119 ATACACGCTGTGTGATGATCATCCGGGCGGCTTGCATCGCCACTGCGTCCCTGACTACTG 1178
Db 241 ATACACGCTGTGTGATGATCATCCGGGCGGCTTGCATCGCCACTGCGTCCCTGACTACTG 300
QY 1179 GTACAAACCTCTCTTCTGGCTCTGTGGGCGCACTCGGCTGTCAACCTGTCTCTACCC 1238
Db 301 GTACAAACCTCTCTTCTGGCTCTGTGGGCGCACTCGGCTGTCAACCTGTCTCTACCC 360
QY 1239 TCTGTGCCACACACAGCTTCCGCGGGGCTTCAACCAAGCTGCTCTGCCCGCCAGAGCTCAA 1298
Db 361 TCTGTGCCACACAGT---CGCGGGCTTACCAAGCTG--TCTGCCCGCCAGAGCTCAA 415
QY 1299 AATCCAGCGCCACACAGCTCTCTGGAGCACTGTGTGAAG 1335
Db 416 AATCCAGCGCCACACAGCTCTCTGGAGCACTGTGTGAAG 452

RESULT 6
LOCUS CB611519 547 bp mRNA linear EST 07-APR-2003
DEFINITION AMGNNUC:NRHY3-00179-H8-A W Rat hypothalamus (10735) Rattus
ACCESSION CB611519
VERSION CB611519.1 GI:29571407
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
TITLE Rattus.
JOURNAL 1 (bases 1 to 547)
COMMENT Amgen EST Program.
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00179 row: h column: 8.
FEATURES
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/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
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/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat
hypothalamus"
ORIGIN
Query Match 29.3%; Score 390.8; DB 6; Length 547;
Best Local Similarity 85.6%; Pred. No. 1e-67;
Matches 471; Conservative 0; Mismatches 72; Indels 7; Gaps 3;
QY 655 CTCAGCATCTACTCAACATCCAGAGGCGCACCCCGCTCCGGCTGGATGGGCTCGAGAG 714
Db 2 CTCAGCATCTACTCAACATCCAGAGGCGCACCCCGCTCCGGCTGGATGGGCGGTGAG 61
QY 715 GCAGCGGCGCGAGCCCCCTCCCGAGGCCCAAGCCCTCAACACCCCA---CCGCTGGC 771
Db 62 ---GCTGGCGCCAGAACCCCGCCAGATGCCAGCCCTCGCCACCTCCAGCTCCCCCAGC 118

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/organism="Rattus norvegicus"
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/strain="Sprague-Dawley"
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/clone="UI-R-B00-agr-c-06-0-UI"
/dev_stage="adult"
/lab_host="DH108 (Life Technologies)"
/clone_lib="UI-R-B00"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The library
(UI-R-B00) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)"

ORIGIN
Query Match      27.8%; Score 371.2; DB 2; Length 499;
Best Local Similarity 90.0%; Pred. No. 8.2e-64;
Matches 397; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 250 GCGGCTTCTGATCCACATGATGATACCTAGTGTGACAGGCGCTGGACCTTCGGC 309
    |||
Db 59 GGTGCTTCTGATCCATTTGATGATGATGATGATGATGATGATGATGATGATGATG 118
    |||
QY 310 CGGGGCTCTGAAGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 369
    |||
Db 119 CGGGGCTCTGAAGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 178
    |||
QY 370 AACATCGTCTCATCAGCTACGACGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 429
    |||
Db 179 AACATCGTCTCATCAGCTATGACGATTCCTGTCAGTCACTCGAGCTGTCCTACAGG 238
    |||
QY 430 GCGCAGAGGTGACACGGCGGGGAGTGGCGGAGATGCTGCTGCTGCTGCTGCTGCTG 489
    |||
Db 239 GCGCAGAGGGGACACGAGAGCGGCGTTCGGAAGATGGCACTGGTGGTGGTGGTGG 298
    |||
QY 490 TTCTGCTCTGCGACACGACCTCTGAGCTGGAGTACTCTGCGGGGAGCTCCATC 549
    |||
Db 299 TTCTGCTGTATGGGCTGCCATCTCTGAGTGGAGTACTCTGCTGGGAGTTCATC 358
    |||
QY 550 CCGAGGGGCACTGCTATGCGAGTTCTTCTACAAGTGTACTTCTCATCAGGCTTC 609
    |||
Db 359 CCGAGGGGCACTGCTATGCTGAGTTCTTCTACAAGTGTACTTCTCATCAGGCTTC 418
    |||
QY 610 ACCCTGGAGTTCTTACGGCTTCTCAGGCTACCTTCTTAACTGAGCATCTACCTG 669
    |||
Db 419 ACCCTCGAGTTCTTACGGCTTCTCAGGCTACCTTCTTAACTGAGCATCTACCTG 478
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QY 670 AACATCCAGAGGCGACCCGC 690
    |||
Db 479 AACATCCAGAGGCGACCCGC 499
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RESULT 9
LOCUS AW669811 519 bp mRNA linear EST 25-APR-2001
DEFINITION 11386 MARC 1B0V Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW669811
VERSION AW669811.1 GI:7526325
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 519)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,

Casas E., Wray, J.E., White, J., Cho, J., Fahrrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-Mckown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
PUBMED 11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAGC
Plate: 108 row: H column: 13
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Location/Qualifiers
1. 519
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/tissue_type="pooled"
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/clone_lib="MARC 1B0V"
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Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
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[illegible]

QY 1065 AGTGGCCAAAGTCGCTGGCGCTCATCGTAGCATCTTTGGGCTCTGCTGGGCCCCATACAC 1124
Db 61 AGTGGCCAAAGTCGCTGGCGCTCATCGTAGCATCTTTGGGCTCTGCTGGGCCCCATACAC 120
QY 1125 GCTGCTGATGATCATCCGGGCGCTGCGCCATGGCCATCGCTGCCCTGACTACTGTGTACGA 1184
Db 121 GCTGCTGATGATCATCCGGGCGCTGCGCCATGGCCATCGCTGCCCTGACTACTGTGTACGA 180
QY 1185 AACCTCTTCTGGCTCTGCTGGGCAACTCGGCTGTCAACCCCTGCTCAACCTCTGCTG 1244
Db 181 AACCTCTTCTGGCTCTGCTGGGCAACTCGGCTGTCAACCCCTGCTCAACCTCTGCTG 240
QY 1245 CCACCACAGCTTCGCGCGGCTTACCAAGTGTCTGCGCCCAAGAGCTCAAAATCCA 1304
Db 241 CCACCACAGCTTCGCGCGGCTTACCAAGTGTCTGCGCCCAAGAGCTCAAAATCCA 300
QY 1305 GCCCCACAGCTCCCTGGAGCACTGTCTGGGAAG 1335
Db 301 GCCCCACAGCTCCCTGGAGCACTGTCTGGGAAG 331

RESULT 12
CO403631
LOCUS
DEFINITION
AGENCOURT 27526928 NIH_MGC 254 Rattus norvegicus cDNA clone
IMAGE:7315203 5', mRNA sequence.
CO403631
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 842)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Express Genomics
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Place: LLNMI5369 row: b column: 01
High quality sequence stop: 637.
Location/Qualifiers
1. .842
/organism="Rattus norvegicus"
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/clone="IMAGE:7315203"
/sex="both"
/tissue_type="Brain - Pooled from several tissues from one
or more individuals"
/lab_host="NIH MGC 254"
/clone_lib="NIH MGC 254"
Note: "Organ: brain/CNS; Vector: pExpress-1; Site 1:
ECORV; Site 2: NotI; RNA obtained from brain tissue of 8
wk old animal. Tissues were snap-frozen and kept at -80C
before RNA extraction and purification (Tri-reagent
method). cDNA was primed using oligo-dT primer:
5'-pGACTAGTTTATCGGAGCGGCGCC(T)25-3' and cloned into
the pECORV/NotI sites of pExpress-1. Size-selection
resulted in an average insert size of 2.18 kb. This
primary library is not normalized (normalized library is

NIH_MGC 255) and was constructed by Express Genomics
(Frederick, MD). Note: this is a NIH_MGC library"

ORIGIN
Query Match 22.1%; Score 294.4; DB 7; Length 842;
Best Local Similarity 90.7%; Pred. No. 1.8e-48;
Matches 313; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 ATGGAGCGCGCGCGCGCGCGCTGACCGCTTCGGGGCGCTGGCGGCGATCGG 60
Db 335 ATGGAGCGCGCGCGCGCGCGCTGATGAACGGCTGGGCGACTCTGGCCGAGAGCGG 394
QY 61 GCGGCGCGCGCGCGCGCGCGCTTCCTCGGCGAGCTGGACCGCGTGTGCGCGCGCTC 120
Db 395 GCGGCTGAGGCGGCGCGCGCGCTTCCTCGGCTGCTGGACCGCTGTCTGGCTGGCTC 454
QY 121 ATGGCGCTGCTCATCGTGGCCACCGCTGTGGGCAACGGCTGGTTCATGCTGCCCTTCG 180
Db 455 ATGGCGCTGCTCATCGTGGCCACAGTACTGGGCAACGGCTGGTTCATGCTGCCCTTCG 514
QY 181 GCGGACTGAGCTCGGCGCGCGCGCGCTTCCTGCTGCTCAACCTGCCATCTCCGAC 240
Db 515 GCGGATTCGAGCTCGGCGCGCGCGCGCTTCCTGCTGCTCAACCTGCCATCTCCGAC 574
QY 241 TTCCTCGTGGCGCGCTTCGTGATCCACCTGTATGACCTAGCTGTGACAGCGCGCTGG 300
Db 575 TTCCTCGTGGCGCGCTTCGTGATCCACCTGTATGACCTAGCTGTGACAGCGCGCTGG 634
QY 301 ACCTTCGCGCGCGCGCTTCGTGCAAGCTGTGGCTGTGTGGACTAC 345
Db 635 AACTTCGCGCGCGCGCTTCGTGCAAGCTGTGGCTGTGTGGACTAC 679

RESULT 13
BY727560 653 bp mRNA linear EST 17-DEC-2002
LOCUS
DEFINITION
BY727560 RIKEN full-length enriched, adult male cortex Mus musculus
cDNA clone B530005H20 5', mRNA sequence.
BY727560
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 653)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasaki, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Sempile, C.A., Setou, M., Shinada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Harai, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shbata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2005, 14:34:44 ; Search time 81 Seconds
(without alignments)
2124.795 Million cell updates/sec

Title: US-10-727-021-7
Perfect score: 2361
Sequence: 1 MERAPPDGLNAGSALAGDA.....LLCPQKLIKPHSSLEHCWK 445

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	2361	100.0	445	3	AAY92218	Aay92218	Human his
2	2361	100.0	445	4	AAB30627	Aab30627	A human h
3	2361	100.0	445	5	ABB79792	Abb79792	Human his
4	2361	100.0	445	6	AAO19746	Aao19746	Human his
5	2361	100.0	445	6	ABP81687	Abp81687	Human his
6	2361	100.0	445	6	ABG74567	Abg74567	Human his
7	2361	100.0	445	6	ABP59931	Abp59931	Human his
8	2361	100.0	445	6	ABO29527	AbO29527	Human wil
9	2361	100.0	445	7	ADD22854	Add22854	Human his
10	2361	100.0	445	8	ADQ89180	Adq89180	Human uro
11	2361	100.0	445	8	ADR31458	Adr31458	Human his
12	2357	99.8	445	2	AAW92975	Aaw92975	Human mac
13	2357	99.8	445	2	AAV06322	Aav06322	Human G p
14	2357	99.8	445	2	AAQ67830	Aaq67830	Human mus
15	2357	99.8	445	6	ABR43667	AbR43667	Human his
16	2357	99.8	445	6	ABP57425	Abp57425	Human his
17	2357	99.8	445	6	ABG76405	Abg76405	Human mus
18	2357	99.8	445	8	ADP66835	Adp66835	Human his
19	2357	99.8	445	8	ADO29494	Ado29494	Human GPC
20	2357	99.8	445	8	ADP76110	Adp76110	Human H3
21	2357	99.8	453	2	AAV22208	Aav22208	Human G-p
22	2357	99.8	453	3	AAI5381	Aai5381	Human G-p
23	2352	99.6	449	4	ABGI2680	Abgi2680	Novel hum
24	2323	98.4	445	6	ABR43668	AbR43668	Monkey hi
25	2323	98.4	445	6	ABP57426	Abp57426	Monkey hi

26	2323	98.4	445	8	ADP76111	Adp76111 Monkey H3
27	2318.5	98.2	714	4	ABGI2681	Abgi2681 Novel hum
28	2366	96.0	431	7	AAO29529	Aao29529 Human H3
29	2320	94.0	445	8	ADF66833	Adf66833 Murine hi
30	2320	94.0	445	8	ADO29495	Ado29495 Mouse GPC
31	2213	93.7	445	2	AAV06323	Aav06323 Rat G pro
32	2213	93.7	445	2	AAQ67831	Aaq67831 Rat musca
33	2213	93.7	445	3	AAI5382	Aai5382 Rat G-pro
34	2213	93.7	445	6	ABR43669	AbR43669 Rat hista
35	2213	93.7	445	6	ABP57427	Abp57427 Rat hista
36	2213	93.7	445	6	ABG76406	Abg76406 Rat musca
37	2213	93.7	445	8	ADP76112	Adp76112 Rat H3 re
38	2136	91.3	409	7	AAO29533	Aao29533 Human H3
39	2146	90.9	415	7	AAO29530	Aao29530 Human H3
40	2061	87.3	395	7	AAO29534	Aao29534 Human H3
41	2057	87.1	413	2	AAV22207	Aav22207 G-protein
42	2057	87.1	413	3	AAI5383	Aai5383 Rat G-pro
43	1941	82.2	379	7	AAO29536	Aao29536 Human H3
44	1919	81.3	365	7	AAO29528	Aao29528 Human H3
45	1915	81.1	365	4	AAQ65580	Aaq65580 Human his

ALIGNMENTS

RESULT 1
AAY92218
ID AAY92218 standard; protein; 445 AA.
XX
AC AAY92218;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human histamine H3 receptor.
XX
KW histamine H3 receptor; biogenic amine receptor homologue.
XX
OS Homo sapiens.
XX
PN WO200020011-A1.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1998; 98WO-US021090.
XX
PR 07-OCT-1998; 98WO-US021090.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Lovenberg TW, Erlander M, Huvar A, Pyati J;
XX
DR WPI: 2000-303632/26.
XX
DR N-PSDB; AAA09061, AAA09062.
XX
PT Novel human histamine H3 receptor polynucleotides and polypeptides used
XX
PS Claim 11; Fig 3; 54pp; English.
XX
CC The human histamine H3 receptor contains the seven conserved hydrophobic
XX
CC domains and specific residues conserved in biogenic amine receptors. The
XX
CC human histamine H3 receptor polynucleotides and polypeptides are used in
XX
CC methods to screen for modulators of receptor activity (claimed). Such
XX
CC agonists and antagonists may prove useful as research tools or may be
XX
CC used as therapeutics to treat disorders directly or indirectly involving
XX
CC histamine receptors (claimed). The characterization of the polynucleotide
XX
CC is useful for forensic analysis, diagnostic applications, and
XX
CC epidemiological studies
XX
SQ Sequence 445 AA;

Query Match 100.0%; Score 2361; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 3.1e-181;

Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPDGLNAGSALAGDAAAGGARGSAWTAVALMALMALLIVATVGLNALVMLAFV 60
DB 1 MERAPDGLNAGSALAGDAAAGGARGSAWTAVALMALMALLIVATVGLNALVMLAFV 60
QY 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
DB 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
DB 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240
DB 181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240
QY 241 GPEPPEAQSPPPPGCGCKQKGHEAMP LHRVGVGEAAVGAAGEATLGGGGGGSV 300
DB 241 GPEPPEAQSPPPPGCGCKQKGHEAMP LHRVGVGEAAVGAAGEATLGGGGGGSV 300
QY 301 ASPTSSSGSSRGTERPRSLKRGSKPSASASLEKRMKQVVSQSFQRFELSRDRKVAKSL 360
DB 301 ASPTSSSGSSRGTERPRSLKRGSKPSASASLEKRMKQVVSQSFQRFELSRDRKVAKSL 360
QY 361 AVISIFGLCWAPYTLMLIIRAACHGHCVPDYWYETSFLLWANSVAVNPVLYPLCHHSFR 420
DB 361 AVISIFGLCWAPYTLMLIIRAACHGHCVPDYWYETSFLLWANSVAVNPVLYPLCHHSFR 420
QY 421 RAFTKLLCPQKLIKOPHSSLEHCWK 445
DB 421 RAFTKLLCPQKLIKOPHSSLEHCWK 445

RESULT 2
AAB30627
ID AAB30627 standard; protein; 445 AA.
XX
AC AAB30627;
XX
DT 19-MAR-2001 (first entry)
DE A human histamine H3 receptor polypeptide.
XX
KW Human; histamine H3 receptor; inflammation; allergy.
XX
OS Homo sapiens.
XX
PN US6136559-A.
XX
PD 24-OCT-2000.
XX
PF 07-OCT-1998; 98US-00167354.
XX
PR 07-OCT-1998; 98US-00167354.
XX
PA (ORTH) ORTHO PHARM CORP.
XX
PI Lovenberg TW, Pyati J, Erlander M, Huvar A;
XX
DR WPI; 2001-023168/03.
DR N-PSDB; AAC62366.
XX
PT Novel DNA molecules useful in gene therapy for the treatment of
PT inflammation or allergy, or for encoding a human histamine H3 receptor
PT and identifying histamine receptor modulators that are useful as
PT therapeutic and diagnostic agents.
XX
PS Example 3; Fig 3; 25pp; English.
XX
CC The present sequence represents human histamine H3 receptor. The
CC histamine H3 receptor DNA molecules are useful for isolating homologues

of receptor, identifying and isolating genomic equivalents of receptor,
and identifying, detecting or isolating mutant forms of the receptor. The
DNA molecules are also useful in gene therapy for the treatment of
inflammation or allergies. The human histamine H3 receptor protein is
useful in identifying modulators of the human histamine H3 receptor,
which in turn are useful as therapeutic and diagnostic agents

XX
SQ Sequence 445 AA;

Query Match 100.0%; Score 2361; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 3.1e-181;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPDGLNAGSALAGDAAAGGARGSAWTAVALMALMALLIVATVGLNALVMLAFV 60
DB 1 MERAPDGLNAGSALAGDAAAGGARGSAWTAVALMALMALLIVATVGLNALVMLAFV 60
QY 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
DB 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
DB 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240
DB 181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240
QY 241 GPEPPEAQSPPPPGCGCKQKGHEAMP LHRVGVGEAAVGAAGEATLGGGGGGSV 300
DB 241 GPEPPEAQSPPPPGCGCKQKGHEAMP LHRVGVGEAAVGAAGEATLGGGGGGSV 300
QY 301 ASPTSSSGSSRGTERPRSLKRGSKPSASASLEKRMKQVVSQSFQRFELSRDRKVAKSL 360
DB 301 ASPTSSSGSSRGTERPRSLKRGSKPSASASLEKRMKQVVSQSFQRFELSRDRKVAKSL 360
QY 361 AVISIFGLCWAPYTLMLIIRAACHGHCVPDYWYETSFLLWANSVAVNPVLYPLCHHSFR 420
DB 361 AVISIFGLCWAPYTLMLIIRAACHGHCVPDYWYETSFLLWANSVAVNPVLYPLCHHSFR 420
QY 421 RAFTKLLCPQKLIKOPHSSLEHCWK 445
DB 421 RAFTKLLCPQKLIKOPHSSLEHCWK 445

RESULT 3
AAB79792
ID AAB79792 standard; protein; 445 AA.
XX
AC AAB79792;
XX
DT 15-NOV-2002 (first entry)
DE Human histamine H3 receptor.
XX
KW Histamine; receptor; G-protein coupled receptor; human. neuroprotective;
KW cardiant; antidepressant; tranquilizer; antiparkinsonian; anorectic;
KW hypotensive; analgesic; antidiabetic; laxative; antiarrhythmic; antiulcer;
KW antiallergic; antiinflammatory.
XX
OS Homo sapiens.
XX
PN US6413743-B1.
XX
PD 02-JUL-2002.
XX
PF 21-AUG-2000; 2000US-00642855.
XX
PR 07-OCT-1998; 98US-00167354.
XX
PA (ORTH) ORTHO PHARM CORP.
XX

PI	Lovenberg TW, Erlander M, Huvar A, Pyati J;	AAO19746 standard; protein; 445 AA.
XX		
DR	WPI; 2002-641560/69.	AAO19746;
DR	N-PSDB; ABN84882.	
XX		
PT	Novel isolated and purified DNA molecule encoding human histamine H3	11-AUG-2003 (first entry)
PT	receptor protein, useful for identifying modulators of human histamine H3	Human histamine receptor subclass H3 protein.
PT	receptor protein activity.	
XX		
PS	Claim 1; Fig 3; 25pp; English.	Human; histamine receptor; H1; H2; H3; antigen; antibody; antiallergic; antiinflammatory; immunosuppressive; allergy; inflammatory disease.
XX		
CC	The present sequence is the protein sequence of the human histamine H3	Homo sapiens.
CC	receptor, a novel G-protein coupled receptor. The sequence is predicted	
CC	from a cDNA clone isolated from a human thalamus cDNA library. It shows	WO200292634-A2.
CC	at least 25% amino acid identity with the human histamine H2 receptor,	
CC	28% with the human histamine H1 receptor, and approximately 25% with the	21-NOV-2002.
CC	family of biogenic amine G-protein coupled receptors. Histamine H3	
CC	receptor cDNA has been expressed in recombinant host cells, which	
CC	produced active recombinant protein. H3 receptor nucleic acids and	27-APR-2002; 2002WO-EP004678.
CC	proteins can be used to identify modulators of H3 receptor activity or	
CC	expression useful as therapeutic or diagnostic agents for central nervous	27-APR-2001; 2001DE-01020816.
CC	system disorders, such as depression, anxiety, psychoses (e.g.	28-MAR-2002; 2002DE-01013916.
CC	schizophrenia), tardive dyskinesia, Parkinson's disease, obesity,	(SCHA/) SCHAEFER U.
CC	hypertension, Tourette's syndrome, sexual dysfunction, drug addiction,	
CC	drug abuse, cognitive disorders, Alzheimer's disease, senile dementia,	PI Schaefer U, Falus A;
CC	obsessive-compulsive behaviour, panic attacks, pain, social phobias,	
CC	eating disorders and anorexia, cardiovascular and cerebrovascular	WPI; 2003-140269/13.
CC	disorders, non-insulin dependent diabetes mellitus, hyperglycaemia,	
CC	constipation, arrhythmia, disorders of the neuroendocrine system, stress	New antibodies specific for histamine receptor proteins, useful for
CC	and spasticity, as well as acid secretion, ulcers, airway constriction,	treating e.g. allergic reactions, which are agonistic and inhibit
CC	asthma, allergy, inflammation and prostate dysfunction	histamine binding.
XX		
SQ	Sequence 445 AA;	Claim 2; Fig 2; 39pp; German.
	Query Match 100.0%; Score 2361; DB 5; Length 445;	
	Best Local Similarity 100.0%; Pred. No. 3.1e-181;	
	Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MERAPPDGPLNAGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVGLNALVMLAFV 60	1 MERAPPDGPLNAGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVGLNALVMLAFV 60
DB	1 MERAPPDGPLNAGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVGLNALVMLAFV 60	1 MERAPPDGPLNAGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVGLNALVMLAFV 60
QY	61 ADSSLRTQNNPFLNLALISDFLVGAFICPLIYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120	61 ADSSLRTQNNPFLNLALISDFLVGAFICPLIYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
DB	61 ADSSLRTQNNPFLNLALISDFLVGAFICPLIYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120	61 ADSSLRTQNNPFLNLALISDFLVGAFICPLIYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY	121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180	121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
DB	121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180	121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
QY	181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNQRTRLRLDGAREAA 240	181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNQRTRLRLDGAREAA 240
DB	181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNQRTRLRLDGAREAA 240	181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNQRTRLRLDGAREAA 240
QY	241 GPEPPEAQSPPPPPGCGWKQKGEAMP LHRVGVGEAAVGAAGEATLGGGGGGSV 300	241 GPEPPEAQSPPPPPGCGWKQKGEAMP LHRVGVGEAAVGAAGEATLGGGGGGSV 300
DB	241 GPEPPEAQSPPPPPGCGWKQKGEAMP LHRVGVGEAAVGAAGEATLGGGGGGSV 300	241 GPEPPEAQSPPPPPGCGWKQKGEAMP LHRVGVGEAAVGAAGEATLGGGGGGSV 300
QY	301 ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSFTQRFSLRDRKVAKSL 360	301 ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSFTQRFSLRDRKVAKSL 360
DB	301 ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSFTQRFSLRDRKVAKSL 360	301 ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSFTQRFSLRDRKVAKSL 360
QY	361 AVIVSIFGLCWAPYTLMLIIIRAAACHGCVDPDYWYETSFWLLWANSVNPVLPCHHSFR 420	361 AVIVSIFGLCWAPYTLMLIIIRAAACHGCVDPDYWYETSFWLLWANSVNPVLPCHHSFR 420
DB	361 AVIVSIFGLCWAPYTLMLIIIRAAACHGCVDPDYWYETSFWLLWANSVNPVLPCHHSFR 420	361 AVIVSIFGLCWAPYTLMLIIIRAAACHGCVDPDYWYETSFWLLWANSVNPVLPCHHSFR 420
QY	421 RAFTKLLCPQKLIKIQPHSSLEHCWK 445	
DB	421 RAFTKLLCPQKLIKIQPHSSLEHCWK 445	
RESULT 4		
AAO19746		

QY 421 RAFTKLLCPQKLIKIOPHSSLEHCWK 445
 DB 421 RAFTKLLCPQKLIKIOPHSSLEHCWK 445

RESULT 5

ABP81687
 ID ABP81687 standard; protein; 445 AA.

XX AC ABP81687;

XX DT 04-MAR-2003 (first entry)

XX DE Human histamine H3 receptor protein SEQ ID NO:549.

XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

XX OS Homo sapiens.

XX PN WO200261087-A2.

XX PD 08-AUG-2002.

XX PF 19-DEC-2001; 2001WO-US050107.

XX PR 19-DEC-2000; 2000US-0257144P.

XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI Burner GC, Roush CL, Brown JP;

XX DR WPI: 2003-046718/04.

XX DR N-PSDB; AB242533.

XX PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.

XX PS Disclosure; Fig 1; 533pp; English.

XX CC The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or

CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention

XX SQ Sequence 445 AA;

Query Match 100.0%; Score 2361; DB 6; Length 445;
 Best Local Similarity 100.0%; Pred. No. 3.1e-181; Indels 0; Gaps 0;
 Matches 445; Conservative 0; Mismatches 0;

QY 1 MERAPPDGLNAGSALAGDAAAAGGARGFSAANTAVLAALMALLIVATVIGNALVWLAFV 60
 DB 1 MERAPPDGLNAGSALAGDAAAAGGARGFSAANTAVLAALMALLIVATVIGNALVWLAFV 60
 QY 61 ADSSLRTQNNFFLLNLAISDFLVGAFCIPLVYVYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
 DB 61 ADSSLRTQNNFFLLNLAISDFLVGAFCIPLVYVYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
 QY 121 SAFNIVLISYDRFLSVTRAVSYRAQQGTRRAVRKMLLWVWLAFLLYGPAILSWEYLSGG 180
 DB 121 SAFNIVLISYDRFLSVTRAVSYRAQQGTRRAVRKMLLWVWLAFLLYGPAILSWEYLSGG 180
 QY 181 SSIPGHCYAEFFVYVYVLTASTLEFFTPFLSVTFNLSIYLNIOQRTLRLLDGAARAA 240
 DB 181 SSIPGHCYAEFFVYVYVLTASTLEFFTPFLSVTFNLSIYLNIOQRTLRLLDGAARAA 240
 QY 241 GPEPPPEAQSPPPPPGCGWQKGGHGEAMPPLHRYGVGEAAVGAAGBATLGGGGGGGGSV 300
 DB 241 GPEPPPEAQSPPPPPGCGWQKGGHGEAMPPLHRYGVGEAAVGAAGBATLGGGGGGGGSV 300
 QY 301 ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMWSSQSFOTRFLSRDRKVAKSL 360
 DB 301 ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMWSSQSFOTRFLSRDRKVAKSL 360
 QY 361 AVIVSIFGLCWAPYTLMLIIRAAACHGCVDPDYWYETSFLLWANSVAVNPVLYPLCHHSFR 420
 DB 361 AVIVSIFGLCWAPYTLMLIIRAAACHGCVDPDYWYETSFLLWANSVAVNPVLYPLCHHSFR 420
 QY 421 RAFTKLLCPQKLIKIOPHSSLEHCWK 445
 DB 421 RAFTKLLCPQKLIKIOPHSSLEHCWK 445

RESULT 6

ABG74567

ID ABG74567 standard; protein; 445 AA.

XX AC ABG74567;

XX DT 08-MAY-2003 (first entry)

XX DE Human histamine receptor H3 protein.

XX KW Human; histamine receptor; H3; antibody; histamine receptor protein;
 KW histamine; extracellular domain; extracellular loop; immunosuppressive;
 KW transmembrane domain; anti-allergic; anti-inflammatory; allergic reaction;
 KW anaphylactic shock; detection.

XX OS Homo sapiens.

XX PN DE10120816-A1.

XX PD 07-NOV-2002.

XX PF 27-APR-2001; 2001DE-01020816.

XX PR 27-APR-2001; 2001DE-01020816.

XX PA (SCHA/) SCHAEFER U.

XX PI Schaefer U;

DR WPI; 2003-168704/17.
XX
PT New antibody specific for histamine receptor protein, useful for treating
PT or preventing e.g. allergy or inflammation, also antigens for its
PT preparation.
XX
XX Claim 2; Fig 2C; 14pp; German.
XX
XX This invention describes a novel antibody that is specific for a
CC histamine receptor protein (HRP), especially human, and is able to
CC inhibit binding of histamine to HRP. The antibody is produced by
CC immunisation with an antigenic polypeptide that comprises (i) an
CC extracellular domain (ECD) having a sequence from the first extracellular
CC loop (ECL) of HRP and optionally a transmembrane domain (TMD) having a
CC sequence from the N-terminus of the third transmembrane region (TMR) of
CC HRP, (ii) ECD having a sequence from the second ECL and optionally a TMD
CC having a sequence from the C-terminus of the fourth TMR or (iii) an ECD
CC having a sequence from the second ECL and optionally a TMD having a
CC sequence from the N-terminus of the 5th TMR. The products of the
CC invention have anti-allergic, anti-inflammatory and immunosuppressive
CC activity. The antibodies are useful for (a) treating or preventing
CC allergic reactions; chronic and/or acute inflammation and/or anaphylactic
CC shock, in humans or animals and (b) diagnostic detection of HRP,
CC especially in immunoassays. This sequence represents the human histamine
CC receptor H3, described in the disclosure of the invention
XX
XX Sequence 445 AA;
XX
Query Match 100.0%; Score 2361; DB 6; Length 445;
Best Local Similarity 100.0%; Pred. No. 3.1e-181;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERAPDGLNAGSAGALAGDAAAAGGARGFSAATVLAALMALLIVATVIGNALVMAFV 60
DB 1 MERAPDGLNAGSAGALAGDAAAAGGARGFSAATVLAALMALLIVATVIGNALVMAFV 60
QY 61 ADSSLRTQNNPFLNLAISDFLVGAFICPLYVPYVLTGRWTGRLGCKLWLVVDYLLCTS 120
DB 61 ADSSLRTQNNPFLNLAISDFLVGAFICPLYVPYVLTGRWTGRLGCKLWLVVDYLLCTS 120
QY 121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLYGPAILLSWEYLSGG 180
DB 121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNNWYFLITASTLEFFTPFLSVTFNNLSIYLNQRTLRDLGAREAA 240
DB 181 SSIPGHCYAEFFYNNWYFLITASTLEFFTPFLSVTFNNLSIYLNQRTLRDLGAREAA 240
QY 241 GPEPPEAQSPPPPPGCGWKQKGHEAMP LHR YGVGEAAVGA BAGEATLGGGGGGSV 300
DB 241 GPEPPEAQSPPPPPGCGWKQKGHEAMP LHR YGVGEAAVGA BAGEATLGGGGGGSV 300
QY 361 AVISIFGLCWAPYTLMLIIRAACHGCVDPYVYETSWLLWANSVNPVLP LCHHSFR 420
DB 361 AVISIFGLCWAPYTLMLIIRAACHGCVDPYVYETSWLLWANSVNPVLP LCHHSFR 420
QY 421 RAFTKLLCPQKLIKIPHSLSHCWK 445
DB 421 RAFTKLLCPQKLIKIPHSLSHCWK 445
RESULT 7
ABP59931
ID ABP59931 standard; protein; 445 AA.
XX
AC ABP59931;
XX
XX 28-AUG-2003 (first entry)
DT
XX

DE Human histamine H3 receptor.
XX
KW Human; histamine H3 receptor; receptor modulator; agonist; nootropic;
KW neuroprotective; cerebroprotective; cardiant; antiasthmatic;
KW immunomodulator; gastrointestinal; antiallergic; antidiabetic;
KW antiinflammatory; hypotensive; antiarrhythmic.
XX
OS Homo sapiens.
XX
XX WO20030404059-A1.
XX
PD 30-MAY-2003.
XX
PF 15-NOV-2001; 2001WO-US045313.
XX
PR 15-NOV-2001; 2001WO-US045313.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Lovenberg T;
XX
XX WPI; 2003-457595/43.
XX
DR N-PSDB; ACC59395.
XX
PT Identifying agonists of recombinant human histamine H3 receptor protein
PT activity, useful for diagnosing and treating H3 receptor-related
PT disorders, such as nervous system disorders, asthma, allergy,
PT hypertension and diabetes.
XX
XX Example 1; Fig 3; 55pp; English.
XX
XX The present invention relates to a method of identifying compounds that
CC are agonists of recombinant human histamine H3 receptor protein activity,
CC comprising combining a compound suspected of being an antagonist of human
CC histamine H3 receptor protein activity with recombinant human histamine
CC H3 receptor protein, and measuring an agonistic effect of the compound on
CC the recombinant human histamine H3 receptor protein. The methods and
CC compositions of the present invention are useful for diagnosing and
CC treating human histamine H3 receptor-related disorders, such as central
CC and peripheral nervous system disorders (depression, anxiety, psychoses,
CC Parkinson's disease, Alzheimer's disease, dementia and tardive
CC dyskinesia), asthma, allergy, diabetes mellitus, inflammation, immune,
CC cardiovascular (hypertension, and arrhythmia) and gastrointestinal
CC disorders. The present sequence is the human histamine H3 receptor
XX
XX Sequence 445 AA;
XX
Query Match 100.0%; Score 2361; DB 6; Length 445;
Best Local Similarity 100.0%; Pred. No. 3.1e-181;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERAPDGLNAGSAGALAGDAAAAGGARGFSAATVLAALMALLIVATVIGNALVMAFV 60
DB 1 MERAPDGLNAGSAGALAGDAAAAGGARGFSAATVLAALMALLIVATVIGNALVMAFV 60
QY 61 ADSSLRTQNNPFLNLAISDFLVGAFICPLYVPYVLTGRWTGRLGCKLWLVVDYLLCTS 120
DB 61 ADSSLRTQNNPFLNLAISDFLVGAFICPLYVPYVLTGRWTGRLGCKLWLVVDYLLCTS 120
QY 121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLYGPAILLSWEYLSGG 180
DB 121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNNWYFLITASTLEFFTPFLSVTFNNLSIYLNQRTLRDLGAREAA 240
DB 181 SSIPGHCYAEFFYNNWYFLITASTLEFFTPFLSVTFNNLSIYLNQRTLRDLGAREAA 240
QY 241 GPEPPEAQSPPPPPGCGWKQKGHEAMP LHR YGVGEAAVGA BAGEATLGGGGGGSV 300
DB 241 GPEPPEAQSPPPPPGCGWKQKGHEAMP LHR YGVGEAAVGA BAGEATLGGGGGGSV 300
QY 301 ASPTSSSSSGSRTGTERPRSLKRGSKSPSASSASLEKRMKMSQSFQRFSLSDRDKVAKSL 360
DB 301 ASPTSSSSSGSRTGTERPRSLKRGSKSPSASSASLEKRMKMSQSFQRFSLSDRDKVAKSL 360

Db 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMWVSQSFTQRFSLDRDKVAKSL 360
 QY 361 AVIVSIFGLCWAPYTLMIIRAAACHGCVDPYVYVTSFWLLWANSVAVNPVLYPLCHHSFR 420
 Db 361 AVIVSIFGLCWAPYTLMIIRAAACHGCVDPYVYVTSFWLLWANSVAVNPVLYPLCHHSFR 420
 QY 421 RAFTKLLCPQKLIKIPHSSLEHCWK 445
 Db 421 RAFTKLLCPQKLIKIPHSSLEHCWK 445

RESULT 8
 ID AAO29527
 XX AAO29527 standard; protein; 445 AA.
 AC AAO29527;
 DT 27-AUG-2003 (first entry)
 XX
 DE Human wild-type H3 receptor (H3a) protein.
 XX
 KW Human; H3 histamine receptor; central nervous system; depression; ulcer;
 KW Tourette's syndrome; sexual dysfunction; drug addiction; cardiovascular;
 KW anxiety; Parkinson's disease; Alzheimer's disease; obesity; arrhythmia;
 KW constipation; gastrointestinal disorder; inflammation; cerebrovascular;
 KW diabetes; hypertension; stress; allergy; prostate dysfunction; asthma;
 KW gene therapy; receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO2003042359-A2.
 PD 22-MAY-2003.
 XX
 PF 04-NOV-2002; 2002WO-US035375.
 XX
 PR 13-NOV-2001; 2001US-0333094P.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Gallagher M, Yates SL;
 XX
 DR WPI; 2003-441792/41.
 DR N-PSDB; AAL59976.
 XX
 PT New polynucleotide encoding a human H3 histamine receptor polypeptide,
 PT useful for diagnosing or treating disorders associated with or modulated
 PT by H3 histamine receptor, e.g. depression, anxiety, obesity, hypertension
 PT or diabetes.
 XX
 PS Example; Page 50-51; 92pp; English.
 XX
 CC The invention relates to splice variants of human H3 histamine receptor
 CC polypeptide and their corresponding polynucleotide sequences. The
 CC invention is useful in diagnosing or treating diseases or disorders
 CC associated with or modulated by the H3 histamine receptor, such as
 CC central nervous system disorders (e.g. depression, anxiety, psychoses,
 CC Parkinson's disease or Alzheimer's disease), obesity, hypertension,
 CC Tourette's syndrome, sexual dysfunction, gastrointestinal disorders (e.g.
 CC constipation), drug addiction, cardiovascular or cerebrovascular
 CC disorders (e.g. arrhythmia), diabetes, stress, ulcers, asthma, allergy,
 CC inflammation and prostate dysfunction. It is also used in gene therapy.
 CC The polypeptide is useful for identifying agonists, antagonists or
 CC inverse agonists of histamine action at the H3 receptor. The present
 CC sequence is human wild-type H3 receptor protein
 SQ Sequence 445 AA;

Query Match 100.0%; Score 2361; DB 7; Length 445;
 Best Local Similarity 100.0%; Pred. No. 3.1e-181;
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPPDGPLNAGALGADAAAGGARGFSAANTAVLAALMALLIVATVIGNALVWLAFV 60

Db 1 MERAPPDGPLNAGALGADAAAGGARGFSAANTAVLAALMALLIVATVIGNALVWLAFV 60
 QY 61 ADSSLRTQNNFLLNLAISDFLVGAFCLPLVVPVYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
 Db 61 ADSSLRTQNNFLLNLAISDFLVGAFCLPLVVPVYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
 QY 121 SAFNIVLISYDRFLSVTRAVSYRAQGGDTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
 Db 121 SAFNIVLISYDRFLSVTRAVSYRAQGGDTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
 QY 181 SSIPEGHCHYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNITQRTRLRDLGAREAA 240
 Db 181 SSIPEGHCHYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNITQRTRLRDLGAREAA 240
 QY 241 GPEPPPEAQPSPPPPPGCGWQKGHGEAMPLHRYGVGEAAVAGBAGATLGGGGGGGGSV 300
 Db 241 GPEPPPEAQPSPPPPPGCGWQKGHGEAMPLHRYGVGEAAVAGBAGATLGGGGGGGGSV 300
 QY 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMWVSQSFTQRFSLDRDKVAKSL 360
 Db 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMWVSQSFTQRFSLDRDKVAKSL 360
 QY 361 AVIVSIFGLCWAPYTLMIIRAAACHGCVDPYVYVTSFWLLWANSVAVNPVLYPLCHHSFR 420
 Db 361 AVIVSIFGLCWAPYTLMIIRAAACHGCVDPYVYVTSFWLLWANSVAVNPVLYPLCHHSFR 420
 QY 421 RAFTKLLCPQKLIKIPHSSLEHCWK 445
 Db 421 RAFTKLLCPQKLIKIPHSSLEHCWK 445

RESULT 9
 ID ADD22854
 XX ADD22854 standard; protein; 445 AA.
 AC ADD22854;
 DT 15-JAN-2004 (first entry)
 XX
 DE Human histamine H3 receptor.
 XX
 KW Human; Histamine H3 receptor; GPCR; G protein-coupled receptor; receptor;
 KW immunogen; depression; anxiety; schizophrenia; Parkinson's disease;
 KW obesity; hypertension; Tourette's syndrome; sexual dysfunction;
 KW drug addiction; drug abuse; cognitive disorder; Alzheimer's disease;
 KW obsessive-compulsive behaviour; panic attack; pain; eating disorder;
 KW anorexia; cardiovascular disorder; cerebrovascular disorder; diabetes;
 KW constipation; arrhythmia; ulcer; asthma; allergy; inflammation;
 KW prostate dysfunction.
 XX
 OS Homo sapiens.
 XX
 PN US6437100-B1.
 XX
 PD 20-AUG-2002.
 XX
 PF 21-AUG-2000; 2000US-00642514.
 XX
 PR 07-OCT-1998; 98US-00167354.
 XX
 PA (ORTH) ORTHO PHARM CORP.
 XX
 PI Lovenberg TW, Erlander M, Huvar A, Pyati J;
 XX
 DR WPI; 2003-810293/76.
 DR N-PSDB; ADD22860, ADD22861.
 XX
 PT New antibody against human histamine H3 receptor, preferably with
 PT receptor antagonist activity, useful for diagnostic purposes and for
 PT treating diseases such as depression, Parkinson's disease, obesity or
 PT hypertension.

PS	Claim 1; SEQ ID NO 7; 25pp; English.	XX	05-AUG-2004.	XX
XX	The invention relates to a monospecific antibody immunologically reactive	PD		
CC	with a protein appearing as ADD22854, where the protein functions as a	XX		
CC	human histamine H3 receptor. The antibody blocks intracellular signaling	PF	14-JAN-2004; 2004WO-US000750.	XX
CC	activity of the human histamine H3 receptor in response to ligand	XX		
CC	binding. The antibody is useful for detecting and quantifying expression	PR	15-JAN-2003; 2003US-0440318P.	
CC	of human histamine H3 receptors, which may be useful for diagnostic,	PR	04-FEB-2003; 2003US-0444783P.	
CC	epidemiological or forensic purposes. The antibody is potentially useful	PR	27-MAR-2003; 2003US-0457901P.	
CC	in treating diseases such as depression, anxiety, schizophrenia,	PR	08-MAY-2003; 2003US-0468775P.	
CC	Parkinson's disease, obesity, hypertension, Tourette's syndrome, sexual	PR	19-MAY-2003; 2003US-0471614P.	
CC	dysfunction, drug addiction or drug abuse, cognitive disorders, sexual	PR	16-JUN-2003; 2003US-0478422P.	
CC	Alzheimer's disease, obsessive-compulsive behaviour, panic attacks, pain,	PR	18-JUL-2003; 2003US-0489529P.	
CC	eating disorders and anorexia, cardiovascular and cerebrovascular	PR	30-JUL-2003; 2003US-0491156P.	
CC	disorders, diabetes, constipation, arrhythmia, ulcers, asthma, allergy,	PR	02-SEP-2003; 2003US-0499594P.	
CC	inflammation, or prostate dysfunction. The present sequence represents	PR	26-SEP-2003; 2003US-0506332P.	
XX	the histamine H3 receptor.	XX	(MILL-) MILLENNIUM PHARM INC.	
SQ	Sequence 445 AA;	PI	Karicheti V, Silos-Santiago I, Eliasof SD;	
	Query Match 100.0%; Score 2361; DB 7; Length 445;	XX		
	Best Local Similarity 100.0%; Pred. No. 3.1e-181;	DR	WPI; 2004-562167/54.	
	Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	N-PSDB; ADQ89179.	
QY	1 MERAPPDGPLNAGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMAFV 60	XX		
DB	1 MERAPPDGPLNAGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMAFV 60	PT	Use of polypeptides related to urological disorders, e.g. 44390, 54181,	
QY	61 ADSSLRTQNNFLLNLAISDFLVGAFICPLYVPYVLTGRWTGRCGLKLVVDVLLCTS 120	PT	211 or for identifying a compound capable of treating a urological	
DB	61 ADSSLRTQNNFLLNLAISDFLVGAFICPLYVPYVLTGRWTGRCGLKLVVDVLLCTS 120	PT	disorder or identifying and treating a subject having a urological	
QY	121 SAFNVLISYDFLSVTRAVSYRAOQDTRRAVRKMLLVWVLAFLYGPAILLSWEYLSGG 180	XX	disorder.	
DB	121 SAFNVLISYDFLSVTRAVSYRAOQDTRRAVRKMLLVWVLAFLYGPAILLSWEYLSGG 180	PS	Claim 1; SEQ ID NO 132; 542pp; English.	
QY	181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGDAREAA 240	XX		
DB	181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGDAREAA 240	CC	The present invention describes the use of polypeptides related to	
QY	241 GPEPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV 300	CC	urological disorders for identifying a compound capable of treating a	
DB	241 GPEPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV 300	CC	urological disorder, identifying a subject having a urological disorder,	
QY	301 ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFRLSRDRKVKSL 360	CC	or treating a subject having a urological disorder. Also described: (1) a	
DB	301 ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFRLSRDRKVKSL 360	CC	method for identifying a compound capable of treating a urological	
QY	361 AVISIFGLCWAPYTLMTIRAAACHGHCVPDYWYETSFWLLWANGAVNPVLYPLCHHSFR 420	CC	disorder; (2) a method for identifying a subject having a urological	
DB	361 AVISIFGLCWAPYTLMTIRAAACHGHCVPDYWYETSFWLLWANGAVNPVLYPLCHHSFR 420	CC	disorder; and (3) a method for treating a subject having a urological	
QY	421 RAFTKLLCPQKLIKIPHSSLEHCWK 445	CC	disorder. The compound has uropathic and cytostatic activities. The	
DB	421 RAFTKLLCPQKLIKIPHSSLEHCWK 445	CC	polypeptides related to urological disorders are useful for identifying a	
	RESULT 10	CC	compound capable of treating a urological disorder, identifying a subject	
ADQ89180	ADQ89180 standard; protein; 445 AA.	CC	having a urological disorder, or treating a subject having a urological	
XX		CC	disorder. Disorders include urinary incontinence and benign prostatic	
AC		CC	hyperplasia. The present sequence represents a human urological disorder	
XX		CC	related protein, which is used in the exemplification of the present	
XX	21-OCT-2004 (first entry)	XX	invention.	
DT		SQ	Sequence 445 AA;	
XX	Human urological disorder related protein 8203 SEQ.132.		Query Match 100.0%; Score 2361; DB 8; Length 445;	
DE			Best Local Similarity 100.0%; Pred. No. 3.1e-181;	
XX	urological disorder; uropathic; cytostatic; urinary incontinence;		Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
KW	benign prostatic hyperplasia; human.			
XX				
OS	Homo sapiens.			
XX				
PN	WO2004065576-A2.			


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Db 301 ASPTSSSSSGTGRPRSLKSGSPASASLEKRMKMWVSQTFQRLSRDRKVAKSL 360
QY 361 AVIVSIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFR 420
Db 361 AVIVSIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFR 420
QY 421 RAFTKLLCPQKLIKPHSSLEHCWK 445
Db 421 RAFTKLLCPQKLIKPHSSLEHCWK 445

RESULT 12
ADNR31458
ID ADR31458 standard; protein; 445 AA.
XX
AC ADR31458;
DT 04-NOV-2004 (first entry)
DE Human histamine H3 receptor protein.
XX
KW Human; Parkinson's disease; obesity; Alzheimer's disease; pain; stress;
KW ulcer; constipation; non-insulin dependent diabetes mellitus;
KW histamine H3 receptor; receptor.
XX
OS Homo sapiens.
XX
PN US2004156845-A1.
PD 12-AUG-2004.
PF 02-DEC-2003; 2003US-00727021.
PR 07-OCT-1998; 98US-00167354.
PR 21-AUG-2000; 2000US-00642852.
XX
PA (LOVE/) LOVENBERG T W.
PA (ERLA/) ERLANDER M.
PA (HUA/) HUVAR A.
PA (PYAT/) PYATI J.
XX
PI Lovenberg TW, Erlander M, Huvar A, Pyati J;
XX
DR WPI; 2004-592726/57.
DR N-PSDB; ADR31456, ADR31457.
XX
PT Novel isolated and purified human histamine H3 receptor protein useful
PT for identifying modulators utilized for treating Parkinson's disease,
PT obesity, Alzheimer's disease, pain, stress or ulcers.
XX
PS Claim 11; SEQ ID NO 7; 26pp; English.
XX
CC The present invention provides a human histamine H3 receptor protein and
CC nucleic acid encoding such protein. The invention is useful for
CC identifying compounds that modulate the activity of human histamine H3
CC receptor. The invention is useful for treating a condition that is
CC mediated by a human histamine H3 receptor in a patient and for treating
CC Parkinson's disease, obesity, Alzheimer's disease, pain, stress, ulcers,
CC constipation and non-insulin dependent diabetes mellitus. The present
CC sequence is a human histamine H3 receptor protein.
XX
SQ Sequence 445 AA;

Query Match 100.0%; Score 2361; DB 8; Length 445;
Best Local Similarity 100.0%; Pred. No. 3.1e-181;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPPDGPINAGLAGDAAAAGARGPSAAWTAVALMALLIVATVIGNALVMLAFV 60
Db 1 MERAPPDGPINAGLAGDAAAAGARGPSAAWTAVALMALLIVATVIGNALVMLAFV 60
QY 61 ADSSLRTQNNFFLLNLAIISDFLVGAFCLPLYPVYLGTGRWTFGRGLCKLWVDVLLCTS 120
```

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Db 61 ADSSLRTQNNFFLLNLAIISDFLVGAFCLPLYPVYLGTGRWTFGRGLCKLWVDVLLCTS 120
QY 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
Db 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFEFLNLSIYLANIOTRRLRLDGAREAA 240
Db 181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFEFLNLSIYLANIOTRRLRLDGAREAA 240
QY 241 GPEPPPEAQPSPPPPPGCGWQKQHGCEAMPLHRYGVGEAAVGAEGEATLGGGGGGGSV 300
Db 241 GPEPPPEAQPSPPPPPGCGWQKQHGCEAMPLHRYGVGEAAVGAEGEATLGGGGGGGSV 300
QY 301 ASPTSSSSSGTGRPRSLKSGSPASASLEKRMKMWVSQTFQRLSRDRKVAKSL 360
Db 301 ASPTSSSSSGTGRPRSLKSGSPASASLEKRMKMWVSQTFQRLSRDRKVAKSL 360
QY 361 AVIVSIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFR 420
Db 361 AVIVSIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFR 420
QY 421 RAFTKLLCPQKLIKPHSSLEHCWK 445
Db 421 RAFTKLLCPQKLIKPHSSLEHCWK 445

RESULT 12
AAW92975
ID AAW92975 standard; protein; 445 AA.
XX
AC AAW92975;
DT 14-MAY-1999 (first entry)
DE Human mACHR-6 protein.
XX
KW mACHR-6; muscarinic acetylcholine receptor 6; disorder; secretion;
KW acetylcholine responsive cell; phosphatidylinositol turn-over;
KW smooth muscle cell contraction; nervous system disorder; glandular;
KW schizo-effective disorder; affective disorder; sleep disorder;
KW movement disorder; eating disorder; drinking disorder; human.
XX
OS Homo sapiens.
XX
PN US5882893-A.
PD 16-MAR-1999.
XX
PF 04-DEC-1997; 97US-00985090.
PR 04-DEC-1997; 97US-00985090.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Goodearl AD;
XX
DR WPI; 1999-214063/18.
DR N-PSDB; AAX02885, AAX02886.
XX
PT Nucleic acids encoding muscarinic acetylcholine receptor 6 - useful for
PT modulating the effects of acetylcholine on acetylcholine responsive
PT cells.
XX
PS Claim 1a; Fig 1A-D; 59pp; English.
XX
CC This invention describes the isolation of a novel human muscarinic
CC acetylcholine receptor 6 (mACHR-6), capable of modulating the effects of
CC acetylcholine on acetylcholine responsive cells. mACHR-6 cDNAs and
CC polypeptides may be used to detect naturally occurring mutations of the
CC mACHR-6 gene and determine if a subject with the mutated gene is at risk
CC of (or is predisposed to have) a mACHR-6 related disorder, modulate cell
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activity mediated by mACHR-6 (e.g. biological processes mediated by phosphatidylinositol turn-over and signalling), secretion of a molecule (e.g. a neurotransmitter or a glandular enzyme), or contraction of a smooth muscle cell, treat disorders mediated by abnormal mAChR-6 activity e.g nervous system disorders (e.g. amnesia, apraxia, agnosia, amnesic dysnomia, amnesic spatial disorientation, Klüver-Bucy syndrome, Alzheimer's related memory loss and learning disability, visual hallucinations, perceptual disturbances, and Lewy body dementia associated delirium), schizo-effective disorders (e.g. schizophrenia with mood swings, and depressive illness), affective disorders, sleep disorders (e.g. REM sleep abnormalities, paradoxical sleep abnormalities, sleep-wakefulness, and body temperature or respiratory depression abnormalities during sleep), pain generating mechanism disorders (e.g. related to irritable bowel syndrome (IBS), or chest pain), movement disorders (e.g. related to Parkinson's disease), eating disorders (e.g. insulin hypersecretion related obesity), drinking disorders (e.g. diabetic polydipsia), smooth muscle related disorders (e.g. IBS, diverticular disease, urinary incontinence, oesophageal achalasia, and chronic obstructive airways disease), cardiac disorders (e.g. pathologic bradycardia or tachycardia, arrhythmia, flutter and fibrillation), and glandular disorders (e.g. xerostomia and diabetes mellitus)

XX SQ Sequence 445 AA;

Query Match 99.8%; Score 2357; DB 2; Length 445;
Best Local Similarity 99.8%; Pred. No. 6.5e-181;
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPDGLNAGALAGAAAGARGPSAWTAVLAALMALLIVATVGLNALVWLAFV 60
DB 1 MERAPDGLNAGALAGAAAGARGPSAWTAVLAALMALLIVATVGLNALVWLAFV 60

QY 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLYYPVYLGTGRTGRLCKLWLVVDYLLCTS 120
DB 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLYYPVYLGTGRTGRLCKLWLVVDYLLCTS 120

QY 121 SAFNVLISYDFLSVTRAVSYRAOQDTRRAVRKMLLVWLAFLLYGPAILLSWEYLSGG 180
DB 121 SAFNVLISYDFLSVTRAVSYRAOQDTRRAVRKMLLVWLAFLLYGPAILLSWEYLSGG 180

QY 181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNTOQRTRELDGAREAA 240
DB 181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNTOQRTRELDGAREAA 240

QY 241 GPEPPEAQSPPPPGCGWKQKGHEAMPRLHRYGVGEAAVCAAGEATLGGGGGGSV 300
DB 241 GPEPPEAQSPPPPGCGWKQKGHEAMPRLHRYGVGEAAVCAAGEATLGGGGGGSV 300

QY 301 ASPTSSSGSSRGTERPSRLKRGSKPSASSASLEKRMKMYVSQFTQRPRLSRDRKVKAKSL 360
DB 301 ASPTSSSGSSRGTERPSRLKRGSKPSASSASLEKRMKMYVSQFTQRPRLSRDRKVKAKSL 360

QY 361 AVIVIFGLCWAPYLLMIIRAACHGCVDPDWYETSFLLWANSVNPVLPCHHSFR 420
DB 361 AVIVIFGLCWAPYLLMIIRAACHGCVDPDWYETSFLLWANSVNPVLPCHHSFR 420

QY 421 RAFTKLCPQKLIKIOPHSSLEHCWK 445
DB 421 RAFTKLCPQKLIKIOPHSSLEHCWK 445

RESULT 13

AAV06322

ID AAY06322 standard; protein; 445 AA.

XX AC AAY06322;

XX DT 06-SEP-1999 (first entry)

XX DE Human G protein coupled receptor flh84g5.

XX KW G protein coupled receptor; flh84g5; human; diagnosis; screening;
KW therapy; antiparkinsonian; nootropic; neuroprotective; neuroleptic;

KW antidepressant; antiarrhythmic; antidiabetic; antiinflammatory;
KW phosphatidylinositol.

OS Homo sapiens.

Key Location/Qualifiers
Domain /note= "transmembrane domain"
Domain /note= "transmembrane domain"
Domain /note= "transmembrane domain"
Domain /note= "transmembrane domain"
Domain /note= "transmembrane domain"
Domain /note= "transmembrane domain"
Domain /note= "transmembrane domain"
Domain /note= "transmembrane domain"

XX W09928470-A1.

PD 10-JUN-1999.

XX 04-DEC-1999; 98WO-US025832.

XX 04-DEC-1997; 97US-00985090.

PR 17-MAR-1998; 98US-00042780.

XX (MILL-) MILLENNIUM PHARM INC.

XX Goodearl ADJ, Gluckmann MA, Xie M, Distefano P;
PI: 1999-394858/33.

DR N-PSDB; AAX59167.

PT New nucleic acid encoding an isolated G-protein coupled receptor useful
PT for treating nervous system related disorders.

XX Claim 8a; Fig 1; 14Opp; English.

XX The present sequence represents a novel human G protein coupled receptor, termed flh84g5, as deduced from a human cerebellum cDNA clone (see AAX59167). The invention provides human, rat and mouse flh84g5 polynucleotides (including polynucleotides encoding the transmembrane regions of flh84g5 and antisense nucleic acid molecules), expression vectors, host cells, transgenic animals, flh84g5 polypeptides and antibodies, and a method of modulating phosphatidylinositol metabolism. The flh84g5 polypeptides can (i) interact with a flh84g5 ligand, such as acetylcholine or carnitine, (ii) interact with a G protein or another protein which naturally binds to flh84g5, (iii) modulate the activity of an ion channel (e.g. a calcium activated chloride channel or a potassium or calcium channel), (iv) modulate cytosolic ion, e.g. calcium concentration, (v) modulate the release of a neurotransmitter, e.g. acetylcholine or carnitine from a neuron, (vi) modulate a flh84g5 ligand response in a responsive cell, (vii) signal ligand binding via phosphatidylinositol turnover, and (viii) modulate phospholipase C activity. The products can be used to treat: disorders mediated by abnormal flh84g5 polypeptide activity such as nervous system related disorders, e.g. amnesia, apraxia, agnosia, amnesic dysnomia, amnesic spatial disorientation, Klüver-Bucy syndrome, Alzheimer's related memory loss and learning disability; disorders affecting consciousness such as visual hallucinations, perceptual disturbances or delirium associated with Lewy body dementia, schizo-effective disorders, schizophrenia with mood swings, depressive illness (primary and secondary); affective disorders such as REM sleep abnormalities in patients suffering from e.g. depression, paradoxical sleep abnormalities, sleep-wakefulness, and body temperature or respiratory depression abnormalities during sleep; disorders affecting pain generation mechanisms e.g. pain related to irritable bowel syndrome or chest pain; movement disorders e.g. Parkinson's disease related movement disorders; eating disorders e.g. insulin hypersecretion related obesity or drinking disorders, e.g.

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CC diabetic polydipsia; smooth muscle related disorders, e.g. irritable
CC bowel syndrome, diverticular disease, urinary incontinence, oesophageal
CC achalasia or chronic obstructive airways disease; cardiac muscle
CC disorders, e.g. pathologic bradycardia or tachycardia, arrhythmia,
CC flutter or fibrillation; and gland related disorder such as xerostomia or
CC diabetes mellitus. The products can also be used for detection, diagnosis
XX and drug screening
XX
SQ Sequence 445 AA;

Query Match          99.8%; Score 2357; DB 2; Length 445;
Best Local Similarity 99.8%; Pred. No. 6.5e-181;
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPPDGLNAGSALAGDAAAAGARGFSAWTAVALAALMALLIVATVGLNALVMLAFV 60
Db 1 MERAPPDGLNAGSALAGDAAAAGARGFSAWTAVALAALMALLIVATVGLNALVMLAFV 60
QY 61 ADSSLRTONNFFLLNLATSDFLVGAFCTPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
Db 61 ADSSLRTONNFFLLNLATSDFLVGAFCTPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
Db 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNNLSIYLNITQRTLRDLGAREAA 240
Db 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNNLSIYLNITQRTLRDLGAREAA 240
QY 241 GREPPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVEAAVGAEGEATLGGGGGGGSV 300
Db 241 GREPPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVEAAVGAEGEATLGGGGGGGSV 300
QY 301 ASPTSSSSSSSGRTSRPSLRKSGKSPASSASLEKRMKMWVSQFTQRFSLRDRKVAKSL 360
Db 301 ASPTSSSSSSSGRTSRPSLRKSGKSPASSASLEKRMKMWVSQFTQRFSLRDRKVAKSL 360
QY 361 AVIVSIFGLCWAPYTLMLIRACHGHCVPDYWYETSWLLWANSVNPVLYPLCHHSFR 420
Db 361 AVIVSIFGLCWAPYTLMLIRACHGHCVPDYWYETSWLLWANSVNPVLYPLCHHSFR 420
QY 421 RAFTKLLCPQKLIQPHSLSHCWK 445
Db 421 RAFTKLLCPQKLIQPHSLSHCWK 445

RESULT 14
AAG67830
ID AAG67830 standard; protein; 445 AA.
XX
AC AAG67830;
XX
DT 20-MAR-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Human muscarinic acetylcholine receptor protein SEQ ID NO:2.
XX
KW Human; muscarinic acetylcholine receptor 6; mAChR-6; detection;
KW antiparkinsonian; nootropic; neuroprotective; neuroleptic; antidiabetic;
KW antidepressant; antiarrhythmic; antiinflammatory; carnitine; pain;
KW G-protein coupled receptor; nervous system related disorder; xerostomia;
KW disorders affecting consciousness; affective disorder; movement disorder;
KW irritable bowel syndrome; drinking disorder; gland related disorder;
KW smooth muscle related disorder; cardiac muscle disorder; eating disorder;
KW diabetes mellitus; diagnosis; drug screening.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 34..59
FT /label= transmembrane_domain
FT 73..91
FT Domain
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FT Domain /label= transmembrane_domain
FT 109..130
FT /label= transmembrane_domain
FT 152..174
FT /label= transmembrane_domain
FT 197..219
FT /label= transmembrane_domain
FT 360..380
FT /label= transmembrane_domain
FT 396..416
FT /label= transmembrane_domain
PN US6093545-A.
XX
PD 25-JUL-2000.
XX
PF 02-OCT-1998; 98US-00165543.
PR 04-DEC-1997; 97US-00985090.
PR 17-MAR-1998; 98US-00042780.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Glucksmann MA, Goodearl ADJ;
XX
DR WPI, 1999-394858/33
DR N-PSDB; AAH44572, AAH44573.
XX
PT New nucleic acid encoding an isolated G-protein coupled receptor useful
PT for treating nervous system related disorders.
XX
PS Claim 1; Fig 1; 64pp; English.
XX
CC The present sequence represents human muscarinic acetylcholine receptor 6
CC (mAChR-6), which is a member of the G family of proteins. mAChR-6 has
CC antiparkinsonian, nootropic, neuroprotective, neuroleptic, antidiabetic
CC antidepressant, antiarrhythmic and antiinflammatory activities. The mAChR
CC -6 protein, is capable of modulating the effects of a G-protein coupled
CC receptor (GPCR) ligand such as acetylcholine or an acetylcholine like
CC molecule such as carnitine, e.g. by modulating phospholipase C
CC signalling/activity. Products from the present invention can be used for
CC treating disorders mediated by abnormal mAChR-6 protein activity such as
CC nervous system related disorders, disorders affecting consciousness,
CC affective disorders such as REM sleep abnormalities, disorders affecting
CC pain generation mechanisms such as pain related to irritable bowel
CC syndrome or chest pain, movement disorders, eating disorders, drinking
CC disorders, smooth muscle related disorders, cardiac muscle disorders, and
CC gland related disorders such as xerostomia or diabetes mellitus. The
CC products can also be used for detection, diagnosis and drug screening.
XX (Updated on 20-MAR-2003 to correct DR field.)
SQ Sequence 445 AA;

Query Match          99.8%; Score 2357; DB 2; Length 445;
Best Local Similarity 99.8%; Pred. No. 6.5e-181;
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPPDGLNAGSALAGDAAAAGARGFSAWTAVALAALMALLIVATVGLNALVMLAFV 60
Db 1 MERAPPDGLNAGSALAGDAAAAGARGFSAWTAVALAALMALLIVATVGLNALVMLAFV 60
QY 61 ADSSLRTONNFFLLNLATSDFLVGAFCTPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
Db 61 ADSSLRTONNFFLLNLATSDFLVGAFCTPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
Db 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNNLSIYLNITQRTLRDLGAREAA 240
Db 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNNLSIYLNITQRTLRDLGAREAA 240
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 19:07:00 ; Search time 24 Seconds
(without alignments)
1784.019 Million cell updates/sec

Title: US-10-727-021-7
Perfect score: 2361
Sequence: 1 MERAPPDGFLNAGALGDA.....LLCPQKXIQPHSSLEHCWK 445
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	724	30.7	390	2 JC7566	histamine H4 recep
2	592	25.1	460	2 I51837	muscarinic recepto
3	592	25.1	460	2 A29514	muscarinic acetyl
4	591.5	25.1	460	2 S09508	muscarinic acetyl
5	587.5	24.9	460	2 A24325	muscarinic acetyl
6	578	24.5	460	2 A31897	muscarinic acetyl
7	553.5	23.4	590	2 S47572	muscarinic acetyl
8	546.5	23.1	590	2 S01114	muscarinic acetyl
9	541	22.9	590	2 S10128	muscarinic acetyl
10	539	22.8	589	2 B29514	muscarinic acetyl
11	536	22.7	479	2 S10127	muscarinic acetyl
12	535	22.7	479	2 S33776	muscarinic acetyl
13	532.5	22.6	478	2 C29514	muscarinic acetyl
14	527.5	22.3	532	2 JT0530	muscarinic acetyl
15	525.5	22.3	466	2 JH0197	muscarinic acetyl
16	525.5	22.3	589	2 A29476	muscarinic acetyl
17	524.5	22.2	466	2 S10856	muscarinic acetyl
18	523.5	22.2	531	2 JT0531	muscarinic acetyl
19	517.5	21.9	466	2 A40972	muscarinic acetyl
20	517.5	21.9	466	2 S10126	muscarinic acetyl
21	512.5	21.7	466	2 A27386	muscarinic acetyl
22	511	21.6	639	2 A55019	muscarinic acetyl
23	505.5	21.4	450	2 A38316	alpha-2-adrenergic
24	504	21.3	490	2 A35546	muscarinic acetyl
25	498.5	21.1	601	2 JH0170	octopamine recepto
26	498.5	21.1	601	2 S12004	tyramine receptor
27	493.5	20.9	461	2 A31237	alpha-2C-adrenergic
28	489.5	20.7	432	2 I50829	alpha 2-adrenocept
29	485.5	20.6	450	2 I49481	alpha-2 adrenergic

30 485 20.5 455 2 S28221 alpha-2-C2 adrener
31 484.5 20.5 450 2 A34169 alpha-2A-adrenergic
32 480.5 20.4 450 2 B40392 alpha-2-adrenergic
33 479 20.3 484 2 S48657 muscarinic acetyl
34 478 20.2 448 2 I51883 alpha-2B-adrenergic
35 478 20.2 458 2 I49480 alpha-2 adrenergic
36 478 20.2 458 2 A40392 alpha-2-adrenergic
37 473 20.0 450 2 A37223 alpha-2B-adrenergic
38 472 20.0 458 2 A37869 alpha-2B-adrenergic
39 469 19.9 453 2 A35642 alpha-2B-adrenergic
40 468.5 19.8 450 2 JH0190 alpha-2-adrenergic
41 468 19.8 491 2 A41632 histamine H1 recep
42 467 19.8 476 2 JC5042 G protein-coupled
43 466 19.7 458 2 A48392 alpha 2C4 adrenoce
44 466 19.7 484 2 S58868 G protein-coupled
45 466 19.7 486 2 JC1415 histamine H1 recep

ALIGNMENTS

RESULT 1
JC7566
histamine H4 receptor, HH4R - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7566
R:Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.
Biochem. Biophys. Res. Commun. 279, 615-620, 2000
A>Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.
A:Reference number: JC7566; MUID: 20568725; PMID:1118334
A:Contents: Leukocyte
A:Accession: JC7566
A:Molecule type: mRNA
A:Residues: 1-390 <NAK>
A:Cross-references: UNIPROT:Q9H3N8; DDBJ:AB045370
C:Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled
C:Genetics:
A:Gene: hh4r
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 30.7%; Score 724; DB 2; Length 390;
Best Local Similarity 38.6%; Pred. No. 1.3e-43;
Matches 164; Conservative 56; Mismatches 131; Indels 74; Gaps 10;

QY 30 SAAWTVLAALMALIVATVLGNALVLAFAVDADSLRTQNNPFLNLAIISDFLVGAFCIP 89
DB 11 SLSTRVTTLAFAFMSLVAFAMLGNALVILAFVVDKMLRHRSSYFFNLAIISDFLVGVISIP 70
QY 90 LYVPVLTGRWTFGRGLCKLMLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAQQGDT 149
DB 71 LYIPHTLF-ENWDFGKEICVFWLTDTLLCTASVYVNLISYDRFLSVTRAVSYRTQHTGV 129
QY 150 RRAVRKMLLVWLAFLLYGPAIL---SWEYLSGGSSIPFG-HCYAEFFNWNFLTASTL 205
DB 130 LKIVTLMVAFLVAPLNGPMLVSESNK-----DEGSECPGFSEWYLAITSPL 181
QY 206 EFFTFFLSVTENLSIYLNIQRTFLRLDGAEEAGPPEPPAQSPPPPCMCWQKG 265
DB 182 BFVIPVILVAFVNMNIY-----WSLWKKD 205
QY 266 HGEAMPLHRYGVGAAGAAEAGEATLGGGGGGSVASPTSSSGSS-----SRGTERPR 318
DB 206 HLSRCQSH-----PGLTAVSSNICGHSFGRSLSSRRSLASAEVSPASFISEQRKRS 257
QY 319 SLKRGSKPSASASLEKMKVMQSFT-----QRFRLSRDKVAKSLAVIVSIFGLCWA 372
DB 258 SLMPSSRTKMSNTTASKMGFSQSDSVALHQREHVELLRARRLAKSLAILLGVEAVCWA 317
QY 373 PYTLMLITRAACHGICVP-DYWYETSFLLWANSVNPVLYPLCHHSFRATKLLCPQK 431
DB 318 PYSLFTIVLSFYSSATGPKSVMYRTAFWLQWNSFNPLLYPLCHKRFQKFLKIFC---- 374


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QY 432 LKIQP 436
Db 375 IKQP 379

RESULT 2
151837
muscarinic receptor - rat
C:Species: Rattus sp. (rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C:Accession: I51837
R:Ali, J.; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roeske
Adv. Exp. Biol. 287, 313-330, 1991
A>Title: The molecular properties of the M1 muscarinic receptor and its regulation of cy
A:Reference number: I51837; MUID:92101806; PMID:1759615
A:Accession: I51837
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-460 <RES>
A:Cross-references: GB:S73971; NID:g241253; PIDN:AAB20705.1; PID:g241254
C:Genetics:
C:Superfamily: vertebrate rhodopsin

Query Match 25.1%; Score 592; DB 2; Length 460;
Best Local Similarity 33.7%; Pred. No. 2.8e-34;
Matches 149; Conservative 66; Mismatches 149; Indels 78; Gaps 17;

QY 33 W-TAVLAALMALLIVATVLGNALVAFVADSSLRNTQNNFFLLNLAISDFLVGAFICPLY 91
Db 23 WQVAFIGITGLSLATVTGNLLVLSFKVNTKLTNNYFLLSLACADLIIGTFSMNLY 82

QY 92 VPIVLTGRWTFGRGLCKLWVDYLLCTSSAFNVLISYDRFLSVTRAVSRAOQGDTRR 151
Db 83 TTYLLMGHWALGTACDLWLALDYVNASVNNLLISFDYFVTRPLSVRAKR-TPRR 141

QY 152 AVRKMLLVMVLAFLYGPAILSWEYLSGSSSIPEGHGCEAMPPLHYGVGEAAVGAEGEATLGGGGGGGVA- 254
Db 142 AALMTGLAWLSFVLWAPAILFWQLVGERIVTLAQCYIQFLSQPIIFGTAMAAFYLP- 200

QY 212 LSVTFNLSIYLNIOQRTRLRLDGAEEA---GPEPP-----PEAQSPPPP 254
Db 201 --VTVM-CTLYWRIYRETNR---ARELAALQGETPGKGGSSSSSSSQPGAGSPES 254

QY 255 PPG-CWGC-----WQKHGCEAMPPLHYGVGEAAVGAEGEATLGGGGGGGVA- 301
Db 255 PPGRCRCRCPRLQLQAYSWKEEBE-----DEGSMEISLTSEGEPP-----GSEVVI 302

QY 302 -----SPTSSSGSSSRGT-ERPRSLKR-----GSKPSASSASLEKMKMVSQSFT 345
Db 303 KMPWVDSQAQPTKQPKSSPNTVKRPTKGRDRGKGQKPRGK-QLAKR----- 352

QY 346 QRFLSRDRKVAKSIAVIVSIFGLCWAPYTLMIIRAAACHGCHVDPDYWYETSFLLWANS 405
Db 353 KTFSLVKEKKAARTLSAILLAPILTPTNIMVLVSTFCK-DCVPETLWELGYLWCYVNS 411

QY 406 AVNPVLYPLCHHSFRRAFTKLL 427
Db 412 TVNPMCYALCNKAFRDTFRLL 433

RESULT 3
A29514
muscarinic acetylcholine receptor M1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A94518; A94293; A37121; A29514
R:Bonner, T.I.
submitted to GenBank, July 1987
A:Reference number: A94518
A:Accession: A94518
A:Molecule type: mRNA
A:Residues: 1-460 <BO1>
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A:Cross-references: UNIPROT:P08482
R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
A>Title: Identification of a family of muscarinic acetylcholine receptor genes.
A:Reference number: A94293; MUID:87263421; PMID:3037705
A:Accession: A94293
A:Molecule type: mRNA
A:Residues: 1-227;338-460 <BO2>
A:Experimental source: cerebral cortex
A>Note: only a part of the protein translation is given; none of the nucleotide sequence
R:Kartenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A>Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invol
A:Reference number: A37121; MUID:90337982; PMID:2380182
A:Accession: A37121
A>Status: preliminary
A:Molecule type: protein
A:Residues: 62-124 <KUR>
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
F:25-50/Domain: transmembrane #status predicted <TM1>
F:62-93/Domain: transmembrane #status predicted <TM2>
F:100-121/Domain: transmembrane #status predicted <TM3>
F:142-168/Domain: transmembrane #status predicted <TM4>
F:187-209/Domain: transmembrane #status predicted <TM5>
F:367-387/Domain: transmembrane #status predicted <TM6>
F:402-420/Domain: transmembrane #status predicted <TM7>
F:2,12/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.1%; Score 592; DB 2; Length 460;
Best Local Similarity 33.7%; Pred. No. 2.8e-34;
Matches 149; Conservative 66; Mismatches 149; Indels 78; Gaps 17;

QY 33 W-TAVLAALMALLIVATVLGNALVAFVADSSLRNTQNNFFLLNLAISDFLVGAFICPLY 91
Db 23 WQVAFIGITGLSLATVTGNLLVLSFKVNTKLTNNYFLLSLACADLIIGTFSMNLY 82

QY 92 VPIVLTGRWTFGRGLCKLWVDYLLCTSSAFNVLISYDRFLSVTRAVSRAOQGDTRR 151
Db 83 TTYLLMGHWALGTACDLWLALDYVNASVNNLLISFDYFVTRPLSVRAKR-TPRR 141

QY 152 AVRKMLLVMVLAFLYGPAILSWEYLSGSSSIPEGHGCEAMPPLHYGVGEAAVGAEGEATLGGGGGGGVA- 211
Db 142 AALMTGLAWLSFVLWAPAILFWQLVGERIVTLAQCYIQFLSQPIIFGTAMAAFYLP- 200

QY 212 LSVTFNLSIYLNIOQRTRLRLDGAEEA---GPEPP-----PEAQSPPPP 254
Db 201 --VTVM-CTLYWRIYRETNR---ARELAALQGETPGKGGSSSSSSSQPGAGSPES 254

QY 255 PPG-CWGC-----WQKHGCEAMPPLHYGVGEAAVGAEGEATLGGGGGGGVA- 301
Db 255 PPGRCRCRCPRLQLQAYSWKEEBE-----DEGSMEISLTSEGEPP-----GSEVVI 302

QY 302 -----SPTSSSGSSSRGT-ERPRSLKR-----GSKPSASSASLEKMKMVSQSFT 345
Db 303 KMPWVDSQAQPTKQPKSSPNTVKRPTKGRDRGKGQKPRGK-QLAKR----- 352

QY 346 QRFLSRDRKVAKSIAVIVSIFGLCWAPYTLMIIRAAACHGCHVDPDYWYETSFLLWANS 405
Db 353 KTFSLVKEKKAARTLSAILLAPILTPTNIMVLVSTFCK-DCVPETLWELGYLWCYVNS 411

QY 406 AVNPVLYPLCHHSFRRAFTKLL 427
Db 412 TVNPMCYALCNKAFRDTFRLL 433

RESULT 4
S09508
muscarinic acetylcholine receptor M1 - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: S09508; S06327; S04326
R:Chapman, C.G.; Browne, M.J.
```

Nucleic Acids Res. 18, 2191, 1990
A>Title: Isolation of the human M1 (Hml) muscarinic acetylcholine receptor gene by PCR
A/Reference number: S09508; NID:90245684; PMID:2336407
A/Accession: S09508
A>Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-460 <CHA>
A/Cross-references: UNIPROT:P11229; EMBL:X52068; NID:g34450; PIDN:CAA36291.1; PID:g34451
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990
R/Allard, W.J.; Sigal, I.S.; Dixon, R.A.F.
Nucleic Acids Res. 15, 10604, 1987
A>Title: Sequence of the gene encoding the human M1 muscarinic acetylcholine receptor.
A/Reference number: S06327; MUID:88098607; PMID:3697105
A/Accession: S06327
A/Molecule type: DNA
A/Residues: 1-460 <ALL>
A/Cross-references: EMBL:X5263; NID:g297405; PIDN:CAA68560.1; PID:g297406
R/Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987
A>Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of three human muscarinic acetylcholine receptor subtypes.
A/Reference number: S04326; MUID:88166632; PMID:3443095
A/Accession: S04326
A/Molecule type: DNA
A/Residues: 1-172, 'M', 174-460 <PER>
A/Cross-references: EMBL:X15263; NID:g32317; PIDN:CAA33334.1; PID:g32318
A/Supertfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C; G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C
F:25-50/Domain: transmembrane #status predicted <TM1>
F:62-93/Domain: transmembrane #status predicted <TM2>
F:100-121/Domain: transmembrane #status predicted <TM3>
F:142-168/Domain: transmembrane #status predicted <TM4>
F:187-209/Domain: transmembrane #status predicted <TM5>
F:367-387/Domain: transmembrane #status predicted <TM6>
F:402-420/Domain: transmembrane #status predicted <TM7>
F:2,12/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.1%; Score 591.5; DB 2; Length 460;
Beat Local Similarity 32.1%; Pred. No. 3e-34;
Matches 151; Conservative 73; Mismatches 158; Indels 89; Gaps 18;
QY 4 APPDGPLNAGALGADAAAGGAGGFSAAW-TAVLAALMALIVATVGLNVALVLAFAVD 62
DB 5 APP-----AVSPNITVTLAPGKG---PMQVAFITGTTGLSLATVGNLVLVLSFKVN 53
QY 63 SSLRTQNNFFLNLAISDFLVGAFICPLYPVPLTGRMTFGRGLCKLWLVLDYLCCTSSA 122
DB 54 TELKTVNNYFLLSLACADLIIGTFSMNLYTYLLGHWALGTLACDLWLDYVNASV 113
QY 123 FNVILSYDRFLSVTRAVSYRAQGDTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGGSS 182
DB 114 MNLLISFDYPSVTRPLSYRAKR-TPRAALMIGLAWLVSFVLWAPAILFWQYLVGERT 172
QY 193 IPEGHCYAEFFNWTFLTASTLEFFTPFLSVTFNLSIYLNIOQRTRLRDLGAREAA-- 240
DB 173 VLAGOCYIQFLSQPIITFTGTAAAFYLP---VTVM-CTLYWRIYRETNR---ARELAAL 225
QY 241 -GPPEP-----PEAOPSPPPPG-CWGC-----WOKGHGEMPLH 273
DB 226 QGSETPGKGGSSSSSSRSQPAEGSPETPPGCCRCRCPRLLOAYSWKEEEB----- 280
QY 274 RYGVGAAGVAGAEATLGGGGGGGVA-----GSEVVKMPMVDPEAQAPKQPPRSPNTVKRPTKG 317
DB 281 DEGSMEISLTSSEGEPP-----GSEVVKMPMVDPEAQAPKQPPRSPNTVKRPTKG 333
QY 318 RS-LKRGSKPASASSASLEKRMKMSQSFQTRFLSRDRKVAKSIAVIVISFGLCWAPYTL 376
DB 334 RDRACKGQKPRGKE-QLAKR-----KTFSLVKEKAARTLSAIIAFLITVTPYNI 383
QY 377 LMIIRAAACHGVDPYVWYETSFWLLWANSVNPVLYPLCHHSFRFAFTKLL 427
DB 384 MVLVSTFCF-DCVPETLWELGYWLCYVNSTINPMCYALCNKAFRDTFRLL 433

RESULT 6

A31897

muscarinic acetylcholine receptor M1 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 24-Nov-1999

C/Accession: A31897

R/Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.

J. Biol. Chem. 263, 18397-18403, 1988

A>Title: Isolation, sequence, and functional expression of the mouse M1 muscarinic acetylcholine receptor.

A/Reference number: A92694; MUID:89054021; PMID:2848036

A/Accession: A31897

A/Molecule type: DNA

RESULT 5

A24325

muscarinic acetylcholine receptor - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004

C/Accession: A24325

R/Kudo, T.; Fukuda, K.; Mikami, A.; Maeda, A.; Takahashi, H.; Mishina, M.; Haga, T.; Haga, T.

Nature 323, 411-416, 1986

A>Title: Cloning, sequencing and expression of complementary DNA encoding the muscarinic acetylcholine receptor.

A/Reference number: A24325; MUID:87014801; PMID:3762692

A/Accession: A24325

A/Molecule type: mRNA

A/Residues: 1-460 <KUB>

A/Cross-references: UNIPROT:P04761; GB:X04413; NID:g1863; PIDN:CAA28003.1; PID:g1866

C/Supertfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C; G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C

F:25-50/Domain: transmembrane #status predicted <TM1>

F:62-93/Domain: transmembrane #status predicted <TM2>

F:100-121/Domain: transmembrane #status predicted <TM3>

F:142-168/Domain: transmembrane #status predicted <TM4>

F:187-209/Domain: transmembrane #status predicted <TM5>

F:367-387/Domain: transmembrane #status predicted <TM6>

F:402-420/Domain: transmembrane #status predicted <TM7>

A;Residues: 1-460 <SHA>
A;Note: the authors translated the codon ATC for residue 119 as Thr
R;Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.
J. Biol. Chem. 264, 6596, 1989
A;Reference number: A92742
A;Contents: annotation; erratum, correct translation of residue 119
C;Superfamily: G protein-coupled rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C; superfamily: G protein-coupled rhodopsin
F;25-50/Domain: transmembrane #status predicted <TM1>
F;62-93/Domain: transmembrane #status predicted <TM2>
F;100-121/Domain: transmembrane #status predicted <TM3>
F;142-168/Domain: transmembrane #status predicted <TM4>
F;187-209/Domain: transmembrane #status predicted <TM5>
F;367-387/Domain: transmembrane #status predicted <TM6>
F;402-420/Domain: transmembrane #status predicted <TM7>

Query Match 24.5%; Score 578; DB 2; Length 460;
Best Local Similarity 33.0%; Pred. No. 2.7e-33;
Matches 146; Conservative 68; Mismatches 150; Indels 78; Gaps 17;

QY 33 W-TAVLAALMALLIVATVGLNVALVAVADSSLTQNNFLLNLAIISDFLVGAFCEIPLY 91
DB 23 WQVAFIGSTGLSLATVGLNLLVLSIKVNTKLTNNVYFLLSLACADLIIGTFESMNL 82
QY 92 VYVLTGRWTEGRLGLKMLVVDYLLCTSSAFNIVLSVDRLSVTRAVSRAQGDTRR 151
DB 83 TTYLLGHWALTLACDLMLADYVNASVWNLJLISFDRLSVTRPLSVRAKR-TPRR 141
QY 152 AVRKMLLVVLAFLYPAILLSWEYLSGGSSIPGEGHCVPEFYNYFLITASTLFFTPF 211
DB 142 AALMIGLAWLVSEVFWAPAILFQWLVGERTVLAQCYIQFLSQIIFGTAWAAFYLP- 200
QY 212 LSVTFNLSIYNQIRRLRLDGBEAA--GPEPP-----PEAQSPPPP 254
DB 201 --VTVM--CTLYWRIYRETNR---ARELAALQSGTTPGKGGSSSSRSRQSGAGSPES 254
QY 255 PPG-CWGC-----WQKHGEAMPLHRYGVGEAAVGAEGEATLGGGGGGGVA- 301
DB 255 PPGRCRCRAPPRLQAVSWKEEBE-----DEGSMESLTSGESEP-----GSEVVI 302
QY 302 -----SPTSSSGSSSROT-RRPSRLK-----GSKPSASSASLEKRMKMWVSQSFT 345
DB 303 KMPWVDPEAAQPTKPPKSPNTVTKKGRDRGKGQKPRGKE-QMAKR----- 352
QY 346 QRFRLSRDRKVAKSLAVISIFGLCWAPYLLMITRAACHGCVDPDYWYETSFLLWANS 405
DB 353 KTFSLVKEKKAARTSAILLAFILTWTPYIMVLVSTFCCK-DCVPETLWELGYLWLCYVNS 411
QY 406 AVNPVLYPLCHHSFRRAFTKLL 427
DB 412 TVNPMCYASCNAFRDHFRLLL 433

RESULT 7
muscarinic acetylcholine receptor m3 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47572
R;Lee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.
Biochim. Biophys. Acta 1223, 151-154, 1994
A;Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 re
A;Reference number: S47572; MUID:94339178; PMID:8061048
A;Accession: S47572
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-590 <LEE>
A;Cross-references: UNIPROT:P41984; EMBL:U08286; NID:G520465; PIDN:AAA51866.1; PID:G5204
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor

Query Match 23.4%; Score 553.5; DB 2; Length 590;
Best Local Similarity 27.1%; Pred. No. 1.8e-31;
Matches 146; Conservative 87; Mismatches 177; Indels 139; Gaps 17;

Matches 149; Conservative 86; Mismatches 175; Indels 139; Gaps 18;
QY 5 PPD-----GPLNASGALAGDAAGGAR----GFSAAWTAV-LAALMALLIVATVGLNVAL 54
DB 30 PPGVTTHFGSYNISRA-AGNLSSPNTGTTSDPLGGHTIMQVVFIAFLTGLVALVTIIGNIL 88
QY 55 VMLAFVADSSLTQNNFLLNLAIISDFLVGAFCEIPLYVYVYVLTGRWTEGRLGLKMLVVD 114
DB 89 VIVAFKVKQKTKVNNYFLLSLACADLIIGVSNMLFTTYIIMKRWALGNLACDLWLSID 148
QY 115 YLLCTSSAFNIVLSYDRFLSVTRAVSRAQGDTRRVRKRLVWVLAFLYLPAILSW 174
DB 149 YVASNASVWNLJLISFDRLSVTRPLSVRAKR-TTKRAGVMIGLAWVISFILWAPAILFW 207
QY 175 EYLSGGSSIPGEGHCVPEFYNYFLITASTLFFTPFLSVTFNLSIYNQIRRLRLD 234
DB 208 QYFVGKRTVPFGCEFIQFLSEPTITFGTAIAAFYMPVTIMTLYWRIYKETEKRTEK-ELA 266
QY 235 GAREAAGPEPPPEAQSPPPP GCGC----- 261
DB 267 GL-QASGTE--AEAEFVHPTGSSRSYSELOQSQMSRRSARRKYGRCHFWFTTKSWKPS 323
QY 262 -----WQKHGEAMPLHRYGVGEAAVGAEA-----GEAT----- 290
DB 324 AEQMDQDSSSDSMNNDAAASLENSASSDEEDIGSETRAIYSIVLKLPGHSTILNKTCL 383
QY 291 -----LGGGG-----GGGSV-----ASPT 304
DB 384 PSSDNLQVPEELGSLERKPSKLTQOQSDMGSGFQSKLPQLQLESADVDTAKASDV 443
QY 305 SSSGSSSGRTGPRSLKRGSKPSASSASLEKRMKMWVSQ-FTORFLS--RDRKVAKSLA 361
DB 444 NSSVGKTTAT-LPLSFK-----EATLAKFAUKTSQITKRKMSLIEKKAQAQILS 494
QY 362 VIVSIFGLCWAPYLLMITRAACHGCVDPDYWYETSFLLWANSVNPVLYPLCHHSFR 421
DB 495 AILLAFILTWTPYIMVLVNTFCD-CLPKTYMNLGYWLCVINSTVNPVCVLCNKTFRN 553
QY 422 AFTKLLCQ 430
DB 554 TFMQLLCCQ 562

RESULT 8
S01114
muscarinic acetylcholine receptor M2, glandular - pig
N;Alternate names: muscarinic acetylcholine receptor III
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S01114
R;Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.
FEBS Lett. 235, 257-261, 1988
A;Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonis
A;Reference number: S01114; MUID:88296835; PMID:3402600
A;Accession: S01114
A;Molecule type: DNA
A;Residues: 1-590 <AKI>
A;Cross-references: UNIPROT:P11483; EMBL:X12712; NID:g1861; PIDN:CAA31215.1; PID:g1862
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmen
F;68-91/Domain: transmembrane #status predicted <TM1>
F;105-125/Domain: transmembrane #status predicted <TM2>
F;143-164/Domain: transmembrane #status predicted <TM3>
F;185-207/Domain: transmembrane #status predicted <TM4>
F;231-252/Domain: transmembrane #status predicted <TM5>
F;493-513/Domain: transmembrane #status predicted <TM6>
F;528-546/Domain: transmembrane #status predicted <TM7>

Query Match 23.1%; Score 546.5; DB 2; Length 590;
Best Local Similarity 26.6%; Pred. No. 5.7e-31;
Matches 146; Conservative 87; Mismatches 177; Indels 139; Gaps 17;
QY 5 PPD-----GPLNASGALAGDAAGGAR----GFSAAWTAV-LAALMALLIVATVGLNVAL 54

Db 30 PPGTVTHFGSYNISQA-AGNFSPNGTSDPLGGHTIMQVVFIAFTGLALVTIIGNIL 88
Qy 55 VMLAFVADSSSLRTQNNFFLLNLAIISDFLVGAFICPLIYPYVLTGRWTFGRGLCKLWLVD 114
Db 89 VIVAFKVNKQLKTVNNYFLLSLACADLIIGVISMLNFTTYIIMRWALGNLACDLWLSD 148
Qy 115 YLLCTSSAFNVLISYDRFLSVTRAVSVRAOQDTRRAVRKMLLVWVLAFLYGPAILSW 174
Db 149 YVASNASVNNLVISFDRYFSITRPLTYRAKR-TTKRAGVMIGLAWVISFVLWAPAILFW 207
Qy 175 EYLSGSSSIPEGHCAEFPYNNYFLITASTLEFFTPFLSVTFNLSIYLNIOQRTRLRD 234
Db 208 QYFVGKRTVPGECEFIQFLSEPTITFGTAIAAFYMPVTIMTILYWRKYKTEKRTK-ELA 266
Qy 235 GAREAAAGPPPEAOPSPPPPGCWG----- 261
Db 267 GL-QASGTE--AEENFVHPTGSSRSCSYELOQSLKRSARKYGRCHFVFTTKSWKPS 323
Qy 262 -----WQKGHEAMPLHRYGVGEAAVGAEA-----GEATLGG----- 294
Db 324 AEQMDQDHSSSDSWNNNDAAASLENSASDEEDIGSETRAIYSIVLKLPGHSTILNSTKL 383
Qy 295 -----GGGSV-----ASPT 304
Db 384 PSSDLQVPEELGTVDLERKASKLQAQKSMDDGGSFQSKLPQLQLESADVDTAKASDV 443
Qy 305 SSSGSSSRGTERPSRLKRGSKPSASSASLEKMKVMSQS--FTQPRLS--RDRKVAKSLA 361
Db 444 NSSVGKTTAT-LPLSFK-----EATLAKFALKTRSQITKRKMSLVKKEKAAQTLS 494
Qy 362 VIVSIFGLCWAPYTLMIIRAACHGCHVDYNYETSFWLLWANSVNPVLYPLCHHSFR 421
Db 495 ALLAFIITWTYNNIMVLNVTFCDS-CIPKTYNGLWLCYINSTVNPVYALCNKTFRT 553
Qy 422 APTKLLCPQ 430
Db 554 TFKMLLLCQ 562

RESULT 9

S10128
muscarinic acetylcholine receptor M4 - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: S10128
R:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987
A:Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of the human M4 muscarinic acetylcholine receptor
A:Reference number: S04326; MUID:88166632; PMID:3443095
A:Accession: S10128
A:Molecule type: DNA
A:Residues: 1-590 <PER>
A:Cross-references: UNIPROT:P20309; EMBL:X15266; NID:g32323; PID:g32324
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein; rhodopsin
F:68-95/Domain: transmembrane #status predicted <TM1>
F:105-131/Domain: transmembrane #status predicted <TM2>
F:143-164/Domain: transmembrane #status predicted <TM3>
F:185-207/Domain: transmembrane #status predicted <TM4>
F:231-252/Domain: transmembrane #status predicted <TM5>
F:493-513/Domain: transmembrane #status predicted <TM6>
F:525-546/Domain: transmembrane #status predicted <TM7>
F:5,6,15,41/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.9%; Score 541; DB 2; Length 590;
Best Local Similarity 26.2%; Pred. No. 1.4e-30;
Matches 145; Conservative 88; Mismatches 178; Indels 142; Gaps 18;

Qy 5 PPD-----GPLNASGLAGDAAAGAR-----GFSNAWTAV-LAALMALLIVATVLGNAL 54

Db 30 PPGTVTHFGSYNVSRA-AGNFSPDGTDDPLDGGHTIMQVVFIAFTGLALVTIIGNIL 88

Qy 55 VMLAFVADSSSLRTQNNFFLLNLAIISDFLVGAFICPLIYPYVLTGRWTFGRGLCKLWLVD 114
Db 89 VIVAFKVNKQLKTVNNYFLLSLACADLIIGVISMLNFTTYIIMRWALGNLACDLWLSD 148
Qy 115 YLLCTSSAFNVLISYDRFLSVTRAVSVRAOQDTRRAVRKMLLVWVLAFLYGPAILSW 174
Db 149 YVASNASVNNLVISFDRYFSITRPLTYRAKR-TTKRAGVMIGLAWVISFVLWAPAILFW 207
Qy 175 EYLSGSSSIPEGHCAEFPYNNYFLITASTLEFFTPFLSVTFNLSIYLNIOQRTRLRD 234
Db 208 QYFVGKRTVPGECEFIQFLSEPTITFGTAIAAFYMPVTIMTILYWRKYKTEKRTK-ELA 266
Qy 235 GAREAAAGPPPEAOPSPPPPGCWG----- 261
Db 267 GL-QASGTE--AEENFVHPTGSSRSCSYELOQSLKRSARKYGRCHFVFTTKSWKPS 323
Qy 262 -----WQKGHEAMPLHRYGVGEAAVGAEA-----GEATLGG----- 294
Db 324 AEQMDQDHSSSDSWNNNDAAASLENSASDEEDIGSETRAIYSIVLKLPGHSTILNSTKL 383
Qy 295 -----GGGSV-----ASPT 304
Db 384 PSSDLQVPEELGTVDLERKASKLQAQKSMDDGGSFQSKLPQLQLESADVDTAKASDV 443
Qy 305 SSSGSSSRGTERPSRLKRGSKPSASSASLEKMKVMSQS--FTQPRLS--RDRKVAKSLA 361
Db 444 NSSVGKTTAT-LPLSFK-----EATLAKFALKTRSQITKRKMSLVKKEKAAQTLS 494
Qy 362 VIVSIFGLCWAPYTLMIIRAACHGCHVDYNYETSFWLLWANSVNPVLYPLCHHSFR 421
Db 495 ALLAFIITWTYNNIMVLNVTFCDS-CIPKTYNGLWLCYINSTVNPVYALCNKTFRT 553
Qy 422 APTKLLCPQ 430
Db 554 TFKMLLLCQ 562

RESULT 10
B29514
muscarinic acetylcholine receptor M3 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: B94518; B94293; B37121; B29514
R:Bonner, T.I.
submitted to GenBank, July 1987
A:Reference number: A94518
A:Accession: B94518
A:Molecule type: mRNA
A:Residues: 1-589 <BO1>
A:Cross-references: UNIPROT:P08483
R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
A:Title: Identification of a family of muscarinic acetylcholine receptor genes.
A:Reference number: A94293; MUID:87263421; PMID:3037705
A:Accession: B94293
A:Molecule type: mRNA
A:Residues: 1-269; 463-589 <BO2>
A:Experimental source: cerebral cortex
A:Note: only a part of the protein translation is given; none of the nucleotide sequence
R:Kurtzsch, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues involved in binding of the antagonist, atropine.
A:Reference number: A37121; MUID:90337982; PMID:2380182
A:Accession: B37121
A:Status: preliminary
A:Molecule type: protein
A:Residues: 104-166 <KUR>
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein; rhodopsin
F:67-90/Domain: transmembrane #status predicted <TM1>
F:104-124/Domain: transmembrane #status predicted <TM2>
F:142-163/Domain: transmembrane #status predicted <TM3>
F:184-206/Domain: transmembrane #status predicted <TM4>

F;230-251/Domain: transmembrane #status predicted <TM5>
F;492-512/Domain: transmembrane #status predicted <TM6>
F;527-545/Domain: transmembrane #status predicted <TM7>
F;615-641/Binding site: carbohydrate (aen) #status predicted

Query Match 22.8%; Score 539; DB 2; Length 589;
Best Local Similarity 26.2%; Pred. No. 1.9e-30;
Matches 135; Conservative 83; Mismatches 168; Indels 130; Gaps 14;

Qy	28	GFSAAWTAV-LAALWALLIVATVGNALVWMAFVADSSLRTONFFLLMLAISDFLUGAF	86
Db	60	GGHTIMQVVFIAFLTGFALVTHIIGILVIVAFKVNKQLKTYNNFTFLSLACADLIIGVI	119
Qy	87	CIPLYVPVLTCRFTFGRGLCKLWLVWDVLLCTSSAFNVLISYDRFLSVTRAVSRAOQ	146
Db	120	SMNLFTYIINRWALGNLACDLWLSIDYVASNASVMNLLVLSFDRYFSITRPLTVRAKR	179
Qy	147	GDTTRAVRKMLLVWVLAFLLYGPAILSWHEYLSGGSSIPEGHCYABFFYNNWFLITASTUE	206
Db	180	TTKRGV-MIGLAWIISFVLMAPALLFWQYFVGKRTVPPGECFIQFLSPBTITTFGTATAIA	238
Qy	207	FFTFPLSVTFENLSIYLNIORTRLRLDGAEEAGPEPPEAQPSPPPPPGCMGC	261
Db	239	FYMPVTIMTILYWRILYKETEKKTK-ELAGL-QASGT--AEAENFVHPGTGSRSSCSYEL	294
Qy	262	-----WQKGHEAMPJHRYGVGBA	280
Db	295	QOQGVKRRRRKYGRCHFWTTSKWKPSAEQMDHSDSDSWNNNDAAASLENSASSDEE	354
Qy	281	AVGAFA-----GEATIG	292
Db	355	DIGSETRAIYISVLKLPQHSSILNSTKLPSSDNLVQSNEDLGTVDVERNAHKLOQKSMG	414
Qy	293	GGGG-----GGSVASPTSSSGSSSRGTGTERPSLKRGSKPSASSASLEKR	336
Db	415	DGDNQCQDFTKLPIQLESADVDTGKTSDTNSSADKTTAT-LPLSEK-----EATLAKR	465
Qy	337	MKNVYSQS-FTQRFLS--RDRKVAKSIAVVISYFGLCWAPYTLMLIRAAACHGCVDPDW	393
Db	466	FALKTRSQITRKRGMSLKEKKAAGTSGAILLAFIITWTFYNNIMVLVNTFCDSC-CLPKTY	524
Qy	394	YETSFLLWANSVNPVLYPLCHHSFRRAF-TKLJC	428
Db	525	WNLGWLYCYINSTNVPVCYALCNKTFRTTEKTLIAC	560

RESULT 11
S10127 muscarinic acetylcholine receptor M3 - human
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C/Accession: S10127
R/Paralata, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987
A/Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of human muscarinic acetylcholine receptor subtypes M1, M2, M3, M4, and M5
A/Reference number: S04326; MUID:88166632; PMID:3443095
A/Accession: S10127

A;Residues: 1-479 <PER>
A;Cross-references: UNIPROT:P08173; EMBL:X15265; NID:g32321; PIDN:CAA33336.1; PID:g32322
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase
F;33-57/Domain: transmembrane #status predicted <TM1>
F;70-94/Domain: transmembrane #status predicted <TM2>
F;106-128/Domain: transmembrane #status predicted <TM3>
F;148-171/Domain: transmembrane #status predicted <TM4>
F;192-216/Domain: transmembrane #status predicted <TM5>
F;401-422/Domain: transmembrane #status predicted <TM6>
F;433-456/Domain: transmembrane #status predicted <TM7>
F;3,8,13/Binding site: carbohydrate (Asn) #status predicted
Query Match 22.7%; Score 536; DB 2; Length 479;
Best Local Similarity 25.6%; Pred. No. 2,5e-30;

Matches	130;	Conservative	101;	Mismatches	150;	Indels	126;	Gaps	14
Qy	9	PLN-ASGALGADAAAGGARGSAATAVLAALMALLIVATVLGNALVMLAFVADSSLR	67						
Db	6	PVNGSSGNQSVRLVTSSSHNRVETVMVFIAATVTSLSLVTVGNILVMLSIKVNRQLQT	65						
Qy	68	QNNFFILNLAISDFLGAFCIPLVYPVVLTCRWTFGRGLCKLMLVDVYLLCTSSAFNIVL	127						
Db	66	VNNYFLPSLACADILIIAGFSNMNLVTVIIKGYWPLGAVVCDMLWLDYVVSNASVMNILLI	125						
Qy	128	ISYDRFLSVTRAVSYRAQOQDTRAVRAKMLLVWVLAFLLYGPAILLSWEYLSGGSSIPBGH	187						
Db	126	ISPDRYFCVTKPLTYPARR-TTKWAGLMIAAAWVLSFVLMAPAILFWQFVVVGKRTVPDQ	184						
Qy	188	CYABEFFNWFLLITASTLEFFTPPLSVTFNLSIYLNIOQRTRL--RLDGAREAG---	241						
Db	185	CFIQFLSNPAVTFGTATAAFYLPVIMTV--LYTHISLASRSVHKHRRPEGEKKAATL	242						
Qy	242	-----PPPPP-----EAQSPS-PPPPGCGWCKQHGHEAMPLHR	274						
Db	243	AFLKSLPMKQSVKKPPGEAREBELRNGKLEAAPPLPPP-----RPV--	287						
Qy	275	YGVEAAVGAEGAEATLGGGGGGSVASPTSSSSSSRGTE-----	315						
Db	288	-----ADKDT-----SNSSSGSATQNTKERPA TELSTTEATTPAMPA	325						
Qy	316	---RPRSLKRGSKPS-----ASSASLEKMKVMQVSSQFT	345						
Db	326	PPLQPRALNPASRWSKIQIVTKQNECVTAIEIVPATPMGRPAANVARKFASIRNQV	385						
Qy	346	QRFR--LSRRKVKAKSLAVIUSIFGLCWAPYTLMIIRAACHGCHVDPDYWTFSEWLLWA	403						
Db	386	RKKQMAAREKVTRTTIFAILLAFILTWTPYNNMVLNVTFCQS-CIPDTVMWSIGYMLCYV	444						
Qy	404	NSAVNPVLYPLCHHSFRRAFTKLLCPQ	430						
Db	445	NSTINPACYALCNATFKKTFHLLLCQ	471						

RESULT 12

S33776

muscarinic acetylcholine receptor m4 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 08-Dec-1993 #sequence revision 01-Dec-1995 #text change 09-Jul-2004

RESULT 12
S33776

muscarinic acetylcholine receptor m4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: S33776, S33135
R:van Koppen, C.J.; Lenz, W.; Nathanson, N.M.
Biochim. Biophys. Acta 1173, 342-344, 1993
A:Title: Isolation, sequence and functional expression of the mouse m4 muscarinic acetylcholine receptor
A:Reference number: S33776; PMID:7916637
A:Accession: S33776
A:Molecule type: DNA
A:Residues: 1-479 <KOP>
A:Cross-references: UNIPROT:P32211; EMBL:X63473; NID:G296913; PIDN:CAA45071.1; PID:G296919
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase A2; GPCR
F:31-56/Domain: transmembrane #status predicted <TM1>
F:69-93/Domain: transmembrane #status predicted <TM2>
F:106-147/Domain: transmembrane #status predicted <TM3>
F:147-170/Domain: transmembrane #status predicted <TM4>
F:192-215/Domain: transmembrane #status predicted <TM5>
F:402-422/Domain: transmembrane #status predicted <TM6>
F:434-455/Domain: transmembrane #status predicted <TM7>

Query Match	22.7%	Score 535;	DB 2;	Length 479;
Best Local Similarity	25.9%;	Pred. No. 3e-30;		
Matches 127; Conservative	96;	Mismatches 174;	Indels 94;	Gaps 11
Qy	9	PLN ^{AS} GALAGDAAAAGGARGFSAWTAVALAAMLLIVATVGLGNALVMIAFVADSSLRTQ	68	
Dd	6	PVN ^{SS} ANQSRLVTVAHNHLETVEMVFIAFTVGSLSLVTGVGILVWLSIKVARQLQTV	65	
Qy	69	NNF ^{LL} NLAISDFLAVGACFIPLYVPYVLIGRWTEGRGLCKLWLVDVYLCLCTSSAFNVILI	128	

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Db 66 NNYFLSLACADLIIGAFSMNLYTYIIKGYWPLGAVVCDLWLDALDYVVSNAVNLLII 125
Qy 129 SYDRFLSVTRAVSVRAOQDTRRAVRKMLLVVLAFLLYGPAILSWELSGSSSIPEGHC 188
Db 126 SFDRYFCVTKPLTYPAR--TTKMGALMTAAAWLSFVLWAPAILFWQFVVGKRTVPDQC 184
Qy 189 YAEFPYNYFLITASTLEFFTPFLSVTFNLSIYLNIOQRTRL---RLDGAREAAAG--- 241
Db 185 FIOFLSNPAVTFGTAAIAAFYLPVVMITV--LYIHISLASRSRVHKKRPEGPKAKTILA 242
Qy 242 -----PEPPP-----EAQSP--PPPCGCGCWKGHGEAMPLHRY 275
Db 243 FLKSPLMKPSIKKPPPGGASREELRNGKLEBAPPALPPP----- 283
Qy 276 GVGEAAVGAEEATLGGGGGGSVASPTSSGSSSRCTE-----RPRSLKRGSKPS- 327
Db 284 --RPVADKDTSNESGSGATQTKERPTELSTTEAATTPALPTLPRTLPNASKWSK 341
Qy 328 -----ASSASLEKRMKMWVSQSFQFR--LSRDRKVAKS 359
Db 342 IQIVTKQTGSECVTAIEIVPATPGMRPAANVARKFASIAARNVKKRQMAARERKVRT 401
Qy 360 LAVIVSIIFGLCWAPYLLMIIRAACHGCHVDYWTETSFVLLWANSVNPVLYPLCHHSF 419
Db 402 IFAILLAFILTWTPYNNVMLVNTFCQS--CIPERVWSIGYMLCYVNSTINPACYALCNATF 460
Qy 420 RRAFTKLCPQ 430
Db 461 KKTFRHLLLCQ 471

RESULT 13
C29514
muscarinic acetylcholine receptor M4 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999
C:Accession: C94518; C94293; E37121; C29514
R:Bonner, T.I.
submitted to GenBank, July 1987
A:Reference number: A94518
A:Accession: C94518
A:Molecule type: mRNA
A:Residues: 1-478 <BOI>
R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
A:Title: Identification of a family of muscarinic acetylcholine receptor genes.
A:Reference number: A94293; MUID:87263421; PMID:3037705
A:Accession: C94293
A:Molecule type: mRNA
A:Residues: 1-233;373-478 <BO2>
A:Experimental source: cerebral cortex
A:Note: only a part of the protein translation is given; none of the nucleotide sequence
R:Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invo
A:Reference number: A37121; MUID:90337982; PMID:2380182
A:Accession: E37121
A>Status: preliminary
A:Molecule type: protein
A:Residues: 68-130 <KUR>
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
F:106-127/Domain: transmembrane #status predicted <TM3>
F:147-170/Domain: transmembrane #status predicted <TM4>
F:192-215/Domain: transmembrane #status predicted <TM5>
F:401-421/Domain: transmembrane #status predicted <TM6>
F:433-454/Domain: transmembrane #status predicted <TM7>
F:8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.6%; Score 532.5; DB 2; Length 478;
Best Local Similarity 25.1%; Pred. No. 4.4e-30;
Matches 139; Conservative 79; Mismatches 165; Indels 125; Gaps 15;
```

```
Matches 127; Conservative 96; Mismatches 158; Indels 125; Gaps 12;
Qy 9 PLNASGALGADAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFVADSSLRHQ 68
Db 6 PVNGSSANQSVRLVTAAHNHLETVEMVFIATVTGSLSLVTVVGNILVMSIKVNRQLQTV 65
Qy 69 NNPFLNLIAISDFLVGAFICIPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVLII 128
Db 66 NNYFLSLGADLIIGAFSMNLYTYIIKGYWPLGAVVCDLWLDALDYVVSNAVNLLII 125
Qy 129 SYDRFLSVTRAVSVRAOQDTRRAVRKMLLVVLAFLLYGPAILSWELSGSSSIPEGHC 188
Db 126 SFDRYFCVTKPLTYPAR--TTKMGALMTAAAWLSFVLWAPAILFWQFVVGKRTVPDQC 184
Qy 189 YAEFPYNYFLITASTLEFFTPFLSVTFNLSIYLNIOQRTRL---RLDGAREAAAG--- 241
Db 185 FIOFLSNPAVTFGTAAIAAFYLPVVMITV--LYIHISLASRSRVHKKRPEGPKAKTILA 242
Qy 242 -----PEPPP-----EAQSP--PPPCGCGCWKGHGEAMPLHRY 275
Db 243 FLKSPLMKPSIKKPPPGGASREELRNGKLEBAPPALPPP-----RPVP----- 287
Qy 276 GVGEAAVGAEEATLGGGGGGSVASPTSSGSSSRCTE----- 315
Db 288 -----DKDTSNENSSGSGATQTKERPTELSTTEAATTPALPAP 325
Qy 316 --RPRSLKRGSKPS-----ASSASLEKRMKMWVSQSFQ 346
Db 326 TLQRTLPNASKWSKIQIVTKQTGNECVTAIEIVPATPGMRPAANVARKFASIAARNVR 385
Qy 347 RFR--LSRDRKVAKS LAVIVSIIFGLCWAPYLLMIIRAACHGCHVDYWTETSFVLLW 404
Db 386 KKRQMAARERKVRTIFAILLAFILTWTPYNNVMLVNTFCQS--CIPETVWSIGYMLCYVN 444
Qy 405 SAVNPVLYPLCHHSFRRAFTKLCPQ 430
Db 445 STINPACYALCNATFKKTRHLLLCQ 470

RESULT 14
JT0530
muscarinic acetylcholine receptor M5 - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
C:Accession: JT0530
R:Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.
Neuron 1, 403-410, 1988
A:Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor
A:Reference number: JT0530; MUID:90166521; PMID:3272174
A:Accession: JT0530
A:Molecule type: DNA
A:Residues: 1-532 <BON>
C:Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neurotr
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
F:67-87/Domain: transmembrane #status predicted <TM2>
F:105-126/Domain: transmembrane #status predicted <TM3>
F:147-169/Domain: transmembrane #status predicted <TM4>
F:192-214/Domain: transmembrane #status predicted <TM5>
F:444-464/Domain: transmembrane #status predicted <TM6>
F:479-498/Domain: transmembrane #status predicted <TM7>
F:8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.3%; Score 527.5; DB 2; Length 532;
Best Local Similarity 27.4%; Pred. No. 1.1e-29;
Matches 139; Conservative 79; Mismatches 165; Indels 125; Gaps 15;
Qy 33 WTAV--LAALMALLIVATVLGNALVMLAFVADSSLRQTNFFLLNLIAISDFLVGAFICIP 91
Db 28 WEVITIAAVTAVVSLITIVGNVLMISPKVNSQLKTNVYLLSLACADLIISGIFSMNLY 87
Qy 92 VPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSVRAOQDTRR 151
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Db 88 TTYILMGRWALGSLADLWLDYVNASVNNLIVISFDRVFSITRPLTYRAKR-TPKR 146
QY 152 AVRKMLLVWVLAFLYGAILLSWEYLSGGSSIPBEGHCVABFFYNNWYFLITASTLEFFTPF 211
Db 147 AGIMIGLAWLISFILWAPAILCWQVLGKRTVPLDECOIQFLSEPTITFTGTAIAAFYIPV 206
QY 212 LSVTFNLSIVLINIQRRTR--LRLDGA----- 236
Db 207 SVMTILYCRITRETEKRTKLADLOGSDSVTKAEKRKAHRAALFRSCLRCRPRPTLAQRER 266
QY 237 -----REAGGP-----PPPEAQSPSPPPPPGCGWCWQ 263
Db 267 NQASWSSRRSTSTTGKFSQATGPSANWAKAEQLTTCSSYPSSSEDEKPADTDPVLQVYV- 325
QY 264 KGHGEAMPRLHYGVGEAAVGAEGATLGGGGGGSVASPTSSSG-----SSRGTER 316
Db 326 KSQKRESP-----GE-BFSAETEETF-----VKAETEKSDYDTPNYLLSPAAHR 370
QY 317 PRSLK-----RGSK-----PSASSASLEKRMKVQSQSFOTRF 348
Db 371 PAKQKVAIKFRLVKAQNGQNTNGCHKVKIMPCFPFVAKBPSYKGLNPNPSHQMTARK 430
QY 349 R--LSRDRKVAKSLAVIYSIFGLCWAPYTLMIIRAACHGHCVDPDYWYETSFWLLWANS 406
Db 431 RWLVKERRKAAQTLSSAILLAFLITWTPYNNIMVLVSTFC-DKCPVPTLWHLGVWLCYVNST 489
QY 407 VNPVLYPLCHHSFRATFK-LLCPOKLK 433
Db 490 VNPICVYALCNRTFRKTFKRMILLCRWKKK 517
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RESULT 15

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JH0197
muscarinic acetylcholine receptor M2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 24-Nov-1999
C:Accession: JH0197; D37121
R:Jai, J.; Bloom, J.W.; Yamamura, H.I.; Roeske, W.R.
Life Sci. 47, 1001-1013, 1990
A:Title: Amplification of the rat m2 muscarinic receptor gene by the polymerase chain re
A:Reference number: JH0197; PMID:91041524; PMID:2172674
A:Accession: JH0197
A:Molecule type: DNA
A:Residues: 1-466 <LA>
R:Kurtendach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invo
A:Reference number: A37121; PMID:90337982; PMID:2380182
A:Accession: D37121
A>Status: preliminary
A:Molecule type: protein
A:Residues: 60-122 <KUR>
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
F:23-48/Domain: transmembrane #status predicted <TM1>
F:61-85/Domain: transmembrane #status predicted <TM2>
F:98-119/Domain: transmembrane #status predicted <TM3>
F:139-162/Domain: transmembrane #status predicted <TM4>
F:184-207/Domain: transmembrane #status predicted <TM5>
F:389-409/Domain: transmembrane #status predicted <TM6>
F:421-442/Domain: transmembrane #status predicted <TM7>
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Query Match 22.3%; Score 525.5; DB 2; Length 466;
Best Local Similarity 26.8%; Pred. No. 1.3e-29;
Matches 130; Conservative 94; Mismatches 170; Indels 91; Gaps 12;
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QY 11 NASGALAGDAAGAGCGFSAATVLAALMALLIVATVGLNALVWLAFAVDSSLRNTONN 70
Db 3 NSTNSNGLAITSYKTFEVVIVLVAGSLV---TIIGNILVWVSKVNRHLQTVNN 59
QY 71 FFLNLALISDFLAVGAFICPLXYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISY 130
```

```
Db 60 YFLSFLACADLIIGVFSNMNLYTLTVIGWPLGPVVCWLWLALDYVSNASVMNLLIISF 119
QY 131 DRFLSVTPAVSYRAOQGDTRAVRKMLLVWLAFLYGPAILSWELSGGSSIPBEGHCV 190
Db 120 DRYFCVTKPLTYPKR-TTKWAGMMIAAAWLSFTLWAPAILFWQFIVGVRTVEGECYI 178
QY 191 EFFYNNWYFLITASTLEFFTPFSLVTFNLSIYLNIQRRTRLRLDGAREAAAGPEPPEAQ 250
Db 179 QFFSNAVTFGTAAAFVLPVIMTV-----LYWHISRAKSRIKKEK-----EPVANQ 228
QY 251 SP PPPPGCGWCQKQKHGEAMP-----LHRYGVGEAAVGAEGEA----- 289
Db 229 DPVSPSLVQGRIVKPNNNMPGCGGLEHKNIQNGKAPRQDGVTCNCVQGEKESNDSTS 288
QY 290 -----TLGGG-----GGGGSVASPTSSS-----G 308
Db 289 VSASNNRRDDEITODENTVSTSLGSHRDDNSKQTCIKIVTKAQKGDVYTPSTTVELVG 348
QY 309 SSSR-GTERPRSLKRGSKPSASSASLEKRMKVQSQSFOTRFSLRDRKVAKSLAVIVSIF 367
Db 349 SSGQNGDEKQNIAR-----KIVKTKQPAKKKPPSPREKKVTRTILAILLAF 396
QY 368 GLCWAPYTLMIIRAACHGHCVDPDYWYETSFWLLWANSVNPVLYPLCHHSFRATFKLL 427
Db 397 IITWAPYNNVMLINTFC-APCIPNTVWTIGYWLVCYNSTINPACVYALCNATFKTKFKHLL 455
QY 428 -CPQK 431
Db 456 MCHYK 460
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Search completed: June 2, 2005, 20:41:15

Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2005, 14:45:59 ; Search time 83 Seconds
(without alignments)
2745.485 Million cell updates/sec

Title: US-10-727-021-7
Perfect score: 2361
Sequence: 1 MERAPPDPLNAGALGDA.....LLCPQKLIQHSSLEHCWK 445

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2357	99.8	445	1 HH3R_HUMAN	Q9Y5N1 homo sapien
2	2323	98.4	445	2 Q865E1	Q865E1 macaca mula
3	2320	94.0	445	1 HH3R_MOUSE	P58406 mus musculus
4	2213	93.7	445	1 HH3R_RAT	Q9GYN8 rattus norv
5	2179	92.3	445	1 HH3R_CAVPO	Q9J135 cavia porce
6	1919	81.3	365	2 Q8WY01	Q8WY01 homo sapien
7	1919	81.3	373	2 Q8WXZ9	Q8WXZ9 homo sapien
8	1521	64.4	301	2 Q8WY00	Q8WY00 homo sapien
9	1521	64.4	309	2 Q8WY00	Q8WY00 homo sapien
10	1223	51.8	247	2 Q8K116	Q8K116 mus musculus
11	1186	50.2	273	2 Q6ZM33	Q6ZM33 brachydanio
12	1137	48.2	210	2 Q8NCH4	Q8NCH4 homo sapien
13	860	36.4	200	2 Q8N150	Q8N150 homo sapien
14	754	31.9	147	2 Q865E3	Q865E3 canis famil
15	724	30.7	390	1 HH4R_HUMAN	Q9H3N8 homo sapien
16	724	30.7	390	2 Q961D9	Q961D9 homo sapien
17	723	30.6	391	2 Q91ZY2	Q91ZY2 mus musculus
18	703	29.8	391	2 Q91ZY1	Q91ZY1 rattus norv
19	694.5	29.4	390	2 Q8WNV9	Q8WNV9 sus scrofa
20	688.5	29.2	389	2 Q91ZY3	Q91ZY3 cavia porce
21	592.5	25.1	460	1 ACW1_MACMU	P56489 macaca mula
22	592	25.1	460	1 ACW1_RAT	P08482 rattus norv
23	591.5	25.1	454	2 Q96RH1	Q96RH1 homo sapien
24	591.5	25.1	460	1 ACW1_HUMAN	P11229 homo sapien
25	587.5	24.9	460	1 ACW1_PIG	P04761 sus scrofa
26	580	24.6	458	2 Q8VH28	Q8VH28 cavia porce
27	580	24.6	460	1 ACW1_MOUSE	P12657 mus musculus
28	570	24.1	110	2 Q865E2	Q865E2 canis famil
29	564	23.9	530	2 Q8VH24	Q8VH24 cavia porce
30	553.5	23.4	590	1 ACW3_BOVIN	P41984 bos taurus
31	548.5	23.2	528	2 Q9PTF6	Q9PTF6 gallus gall

RESULT 1

ID	HH3R_HUMAN	STANDARD;	PRT;	445 AA.
AC	Q9Y5N1: Q9GZX2: Q9H4K8;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DE	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Histamine H3 receptor (HH3R) (G protein-coupled receptor 97) .			
GN	Name=HRH3; Synonyms=GPCR97;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Thalamus;			
RX	MEDLINE=99278519; PubMed=10347254;			
RA	Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,			
RA	Huvar A., Jackson M.R., Erlander M.G.;			
RT	"Cloning and functional expression of the human histamine H3			
RT	receptor."			
RL	Mol. Pharmacol. 55:1101-1107(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.			
RX	MEDLINE=20568725; PubMed=1118334; DOI=10.1006/bbr.2000.4008;			
RA	Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;			
RT	"Molecular cloning and characterization of a new human histamine			
RT	receptor, HH4R."			
RL	Biochem. Biophys. Res. Commun. 279:615-620(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5; 6 AND 7).			
RC	TISSUE=Thalamus;			
RX	MEDLINE=21181559; PubMed=11284713; DOI=10.1042/0264-6021:3550279;			
RA	Coge P., Guenin S.-P., Audinot V., Renouard-Try A., Beauverger P.,			
RA	Macia C., Ouyri C., Nagel N., Riquie H., Boutin J.A., Galizzi J.-P.;			
RT	"Genomic organization and characterization of splice variants of the			
RT	human histamine H3 receptor."			
RL	Biochem. J. 355:279-288(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME			
RP	VAL-280.			
RC	TISSUE=Blood;			
RX	MEDLINE=21953383; PubMed=11956964; DOI=10.1007/s00702000036;			
RA	Wiedemann P., Boenisch H., Oerters F., Brues M.;			
RT	"Structure of the human histamine H3 receptor gene (HRH3) and			
RT	identification of naturally occurring variations."			
RL	J. Neural Transm. 109:443-453(2002).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 3).			
RA	Ullmer C., Zirwes E., Lubbert H.;			
RT	"Cloning and functional expression of the human histamine H3S			
RT	receptor."			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
RN	[6]			

P11483 sus scrofa
Q66118 fugu rubrip
Q71286 brachydanio
P20309 homo sapien
Q9n2a4 pan troglod
Q9n2a2 pongo pygma
Q9n2a3 gorilla gor
Q967g9 homo sapien
P08483 rattus norv
Q8Vh25 cavia porce
Q967g8 homo sapien
P08173 homo sapien
P32111 mus musculus
P56490 macaca mula


```

DR PRINTS: PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G PROTEIN RECP F1.1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1.2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 39 Extracellular (Potential).
FT TRANSMEM 40 60 Potential.
FT DOMAIN 61 70 Cytoplasmic (Potential).
FT TRANSMEM 71 91 Potential.
FT DOMAIN 92 108 Extracellular (Potential).
FT TRANSMEM 109 129 Potential.
FT DOMAIN 130 156 Cytoplasmic (Potential).
FT TRANSMEM 157 177 Potential.
FT DOMAIN 178 196 Extracellular (Potential).
FT TRANSMEM 197 217 Potential.
FT DOMAIN 218 359 Cytoplasmic (Potential).
FT TRANSMEM 360 380 Potential.
FT DOMAIN 381 396 Extracellular (Potential).
FT TRANSMEM 397 417 Potential.
FT DOMAIN 418 445 Cytoplasmic (Potential).
FT DOMAIN 20 23 Poly-Ala.
FT CARBOHYD 11 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 445 AA; 48541 MW; B8D406E29E1F3C5F CRC64;

Query Match 94.0%; Score 2220; DB 1; Length 445;
Best Local Similarity 93.9%; Pred No. 1.7e-118;
Matches 419; Conservative 8; Mismatches 17; Indels 2; Gaps 2;

QY 1 MERAPPDGLNAGALAGADAAAAGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV 60
Db 1 MERAPPDGLNAGALAGADAAAAGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV 60
QY 61 ADSSLRTQNNFLLNLATSDFLVGFACFPLYPYVLTGRTWTFGRGLCKLWLVVDYLLCTS 120
Db 61 ADSSLRTQNNFLLNLATSDFLVGFACFPLYPYVLTGRTWTFGRGLCKLWLVVDYLLCAS 120
QY 121 SAFNVLISYDFLSVTRAVSRAOQDTRRAVRKMLLWVLAFLLYGPAILSWELSGG 180
Db 121 SVFNVLISYDFLSVTRAVSRAOQDTRRAVRKMLWVLAFLLYGPAILSWELSGG 180
QY 181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNIOQRTRLRDGLAREAA 240
Db 181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNIOQRTRLRDGLGRE-A 239
QY 241 GPEPPEAQSPPP-PPGCGWGQKGGHEAMPLHRYGVGEAAVGAEGEATLGGGGGGGS 299
Db 240 GPEPPEAQSPPPAPPSCWGCWPKGGHEAMPLHRYGVGEAGPVETGEAGLGGGGGGGA 299
QY 300 VASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKWVSQSTQRFRLSRDRKVAKS 359
Db 300 AASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKWVSQSTQRFRLSRDRKVAKS 359
QY 360 LAVIVSIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFMLLWANSVNPVLYPLCHHSF 419
Db 360 LAVIVSIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFMLLWANSVNPVLYPLCHYSF 419
QY 420 RRAFTKLLCPQKLTQPHSSLEHCWK 445
Db 420 RRAFTKLLCPQKLVQPHGSLQCKW 445

RESULT 4
HH3R_RAT STANDARD; PRT; 445 AA.
AC Q9QYN8; Q9QYN6; Q9QYN7; Q9QYN9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Histamine H3 receptor (RH3R).
GN Name=HrH3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;

RN [1] SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Hypothalamus;
RC MEDLINE=20330707; PubMed=10869375;
RA Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;
RT "Cloning of rat histamine H3 receptor reveals distinct species pharmacological profiles.";
RL J. Pharmacol. Exp. Ther. 293:771-778(2000).
RN [2] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP TISSUE=Striatum;
RC MEDLINE=21016732; PubMed=11130725; DOI=10.1038/35048583;
RA Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,
RT Stark H., Schunack W., Ganellin C.R., Schwartz J.-C., Arrang J.-M.;
RT "High constitutive activity of native H3 receptors regulates histamine neurons in brain.";
RL Nature 408:860-864(2000).
RN [3] SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RP Itadani H., Takimura T., Nakamura T., Ohta M.;
RT "Cloning of a novel G protein-coupled receptor.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [4] TISSUE SPECIFICITY.
RP MEDLINE=99278519; PubMed=10347254;
RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
RA Huvar A., Jackson M.R., Erlander M.G.;
RT "Cloning and functional expression of the human histamine H3 receptor.";
RL Mol. Pharmacol. 55:1101-1107(1999).
CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylylate cyclase and displays high constitutive activity (spontaneous activity in the absence of agonist).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=H3L;
CC IsoId=Q9QYN8-1; Sequence=Displayed;
CC Name=2; Synonyms=H3S;
CC IsoId=Q9QYN8-2; Sequence=VSP_001887;
CC Name=3;
CC IsoId=Q9QYN8-3; Sequence=VSP_001888;
CC Name=4;
CC IsoId=Q9QYN8-4; Sequence=VSP_001889;
CC -!- TISSUE SPECIFICITY: Expressed abundantly in brain, most notably throughout the thalamus, the ventromedial hypothalamus and the caudate nucleus. Isoform 1 is largely predominant in all tissues.
CC -!- MISCELLANEOUS: Proxifan acts as a potent neutral antagonist while thioperamide, ciproxifan and FUB465 act as potent inverse agonists.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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EMBL; AF237919; AAF82086.1; -
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EMBL; AB015646; BAA88766.1; -
EMBL; AB015646; BAA88767.1; -
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EMBL; AB015646; BAA88769.1; -
EMBL; AB015646; BAA88770.1; -
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EMBL; AB015646; BAA88772.1; -
EMBL; AB015646; BAA88773.1; -
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EMBL; AB015646; BAA88775.1; -
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EMBL; AB015646; BAA88777.1; -
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EMBL; AB015646; BAA88779.1; -
EMBL; AB015646; BAA88780.1; -
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EMBL; AB015646; BAA88783.1; -
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EMBL; AB015646; BAA88787.1; -
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EMBL; AB015646; BAA88797.1; -
EMBL; AB015646; BAA88798.1; -
EMBL; AB015646; BAA88799.1; -
EMBL; AB015646; BAA88800.1; -
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DR	PROSITE; PS00237; G-PROTEIN RECF F1_1; 1.	
DR	PROSITE; PS0262; G-PROTEIN RECF F1_2; 1.	
KW	Alternative splicing; G-protein coupled receptor; Glycoprotein;	
KW	Transmembrane.	
FT	DOMAIN 1	Extracellular (Potential).
FT	TRANSMEM 40	Potential.
FT	DOMAIN 61	Cytoplasmic (Potential).
FT	TRANSMEM 71	Potential.
FT	DOMAIN 92	Extracellular (Potential).
FT	TRANSMEM 109	Potential.
FT	DOMAIN 130	Cytoplasmic (Potential).
FT	TRANSMEM 157	Potential.
FT	DOMAIN 178	Extracellular (Potential).
FT	TRANSMEM 197	Potential.
FT	DOMAIN 218	Cytoplasmic (Potential).
FT	TRANSMEM 360	Potential.
FT	DOMAIN 381	Extracellular (Potential).
FT	TRANSMEM 397	Potential.
FT	DOMAIN 418	Cytoplasmic (Potential).
FT	DOMAIN 20	Poly-Ala.
FT	CARBOHYD 11	N-linked (GlcNAc..) (Potential).
FT	VARSPLIC 274	Missing (in isoform 2).
FT	VARSPLIC 274	Missing (in isoform 3 and isoform 4).
FT	VARSPLIC 393	FTID=VSP 001888.
FT	VARSPLIC 445	WYTSFWLLWANSVNPVLYPLCHVSPFRAPTKLCPQKX
FT	VARSPLIC 445	QPHGSLQCKW -> CYERGLKLEALLLLWPFSGWR
FT	VARSPLIC 445	RKHVCELDVPMFQNCRCRGWICRGCLPRPPSVLQ
FT	VARSPLIC 445	LPAPRQLLPAPPGELGRWPCPCPCTIRGWVNG
FT	VARSPLIC 445	(in isoform 4).
FT	VARSPLIC 445	FTID=VSP 001889.
FT	VARSPLIC 445	63DFEFC21758FE5B CRC64;
FT	VARSPLIC 445	SEQUENCE 445 AA; 48588 MW; 63DFEFC21758FE5B CRC64;
Qy	Query Match	93.7%; Score 2213; DB 1; Length 445;
Db	Best Local Similarity	93.5%; Pred. No. 4.3e-118;
Db	Matches 417; Conservative	9; Mismatches 18; Indels 2; Gaps 2;
Qy	1	MERAPPDGLNAGSALAGDAAGARGFSAAWTAALWALLIVATVGLNALVMAFV 60
Db	1	MERAPPDGLNAGSALAGDAAGARGFSAAWTAALWALLIVATVGLNALVMAFV 60
Qy	61	ADSSLRQNNFLLNLAIISDFLVGAFCLPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
Db	61	ADSSLRQNNFLLNLAIISDFLVGAFCLPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCAS 120
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Qy	181	SSIPGHCHYAEFFNYNYFLITASTLEFPPLSVTFNLSYLNQTRRLDGLGAREAA 240
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Qy	241	GPEPPEAQPPPP-PPGCGWQKQGHGEMPLHRYGVGEAAVGAEEATLGGGGGGGS 299
Db	240	GPEPPEAQPPPP-PPGCGWQKQGHGEMPLHRYGVGEAGPVGVEAGALGGGGGGA 299
Qy	300	VASPTSSSGSSSGRTERPRSLKRGSKPSASSASLEKRMKWSQSQTFRFLSRDRKVAKS 359
Db	300	AASPTSSSGSSSGRTERPRSLKRGSKPSASSASLEKRMKWSQSQTFRFLSRDRKVAKS 359
Qy	360	LAVIVSIIGLCWAPYTLMLITRAACHGCVDPDYWTYTSFWLLWANSVNPVLYPLCHHSF 419
Db	360	LAVIVSIIGLCWAPYTLMLITRAACHGCRIDYWTYTSFWLLWANSVNPVLYPLCHYSF 419
Qy	420	RAFTKLCPOKLTQPHSSLEHCWK 445
Db	420	RAFTKLCPOKLVQPHGSLQCKW 445
RESULT	5	

HH3R_CAVPO	STANDARD;	PRT;	445 AA.
ID	HH3R_CAVPO		
AC	Q9J135; Q9J136;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Histamine H3 receptor (HH3R).		
GN	Name=HRH3;		
OS	Cavia porcellus (Guinea pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.		
OX	NCBI_TaxID=10141;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).		
RC	TISSUE=Brain;		
RX	MEDLINE=20218440; PubMed=10757514;		
RA	Tardivel-Lacombe J., Rouleau A., Heron A., Morisset S., Pillot C.,		
RA	Cochois V., Schwartz J.-C., Arrang J.-M.;		
RT	"Cloning and cerebral expression of the guinea pig histamine H3		
RT	receptor: evidence for two isoforms."		
RL	Neuroreport 11:755-759(2000).		
CC	-!- FUNCTION: The H3 subclass of histamine receptors could mediate the		
CC	histamine signals in CNS and peripheral nervous system. Signals		
CC	through the inhibition of adenylyl cyclase and displays high		
CC	constitutive activity (spontaneous activity in the absence of		
CC	agonist).		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-!- ALTERNATIVE PRODUCTS:		
CC	Name=Long; Synonyms=H3L;		
CC	Isoid=Q9J135-1; Sequence=Displayed;		
CC	Name=Short; Synonyms=H3S;		
CC	Isoid=Q9J135-2; Sequence=VSP 001890;		
CC	-!- TISSUE SPECIFICITY: Expressed widely and abundantly throughout the		
CC	brain. Highly expressed in discrete neuronal populations such as		
CC	pyramidal cells in cerebral cortex or cerebellar Purkinje cells.		
CC	-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/		
CC	or send an email to license@isb-sib.ch).		
CC	EMBL; AF267537; AAF78947.1; -		
DR	EMBL; AF267538; AAF78950.1; -		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	InterPro; IPR003980; H3 receptor.		
DR	Pfam; PF00001; 7tm.1.1;		
DR	PRINTS; PR00237; GPCRHDOPSN.		
DR	PRINTS; PR01471; HISTAMINEH3R.		
DR	PROSITE; PS00237; G-PROTEIN RECF F1_1; 1.		
DR	PROSITE; PS0262; G-PROTEIN RECF F1_2; 1.		
KW	Alternative splicing; G-protein coupled receptor; Glycoprotein;		
KW	Transmembrane.		
FT	DOMAIN 1	Extracellular (Potential).	
FT	TRANSMEM 41	Potential.	
FT	DOMAIN 62	Cytoplasmic (Potential).	
FT	TRANSMEM 72	Potential.	
FT	DOMAIN 93	Extracellular (Potential).	
FT	TRANSMEM 110	Potential.	
FT	DOMAIN 131	Cytoplasmic (Potential).	
FT	TRANSMEM 158	Potential.	
FT	DOMAIN 179	Extracellular (Potential).	
FT	TRANSMEM 198	Potential.	
FT	DOMAIN 219	Cytoplasmic (Potential).	
FT	TRANSMEM 360	Potential.	
FT	DOMAIN 381	Extracellular (Potential).	
FT	TRANSMEM 399	Potential.	
FT	DOMAIN 420	Cytoplasmic (Potential).	
FT	DOMAIN 20	Poly-Ala.	

FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).
FT VARGPLIC 276 305 Missing (in isoform Short).
FT /FTId=VSP 001880.
SQ SEQUENCE 445 AA; 48734 MW; BA2206A3887189A0 CRC64;
Query Match 92.3%; Score 2179; DB 1; Length 445;
Best Local Similarity 92.8%; Pred. No. 3.7e-116;
Matches 415; Conservative 10; Mismatches 18; Indels 4; Gaps 3;
QY 1 MERAPPDGLNAGSAGALAGD-AAAAGGARGFSAWTAVALAALLMALLIVATVGLNALVMLAF 59
DB 1 MERAPPDGLNAGSAGALAGD-AAAAGGARGFSAWTAVALAALLMALLIVATVGLNALVMLAF 60
QY 60 VADSSLRQNNFFLNLAISDFLVGAFICPLVVPVLTGRWTFGRGLCKMLVVDVLLCT 119
DB 61 VADSSLRQNNFFLNLAISDFLVGAFICPLVVPVLTGRWTFGRGLCKMLVVDVLLCT 120
QY 120 SSANFNLISYDRFLSVTRAVSYRAQQGDTTRAVRKMVLVWVLAFLLYGPAILLSWEYLSG 179
DB 121 SSVFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMVLVWVLAFLLYGPAILLSWEYLSG 180
QY 180 GSSIEGHCYAEFFNNWYFLITASTLEFPTPLSVTFNLSIYLNQRRTRLRLDGAEEA 239
DB 181 GSSIEGHCYAEFFNNWYFLITASTLEFPTPLSVTFNLSIYLNQRRTRLRLDGAEEA 240
QY 240 AGPEPPPEAQPSP-PPPGCWGCKGHEAMPLHRYGVGEAAVGAEGEATLGGGGGGG 298
DB 241 AGPDLPLQAQSP-PPPGCWGCKGHEAMPLHRYGVGEAAVGAEGEATLGGGGGGG 298
QY 299 SVAFTSSSGSSSGRTERPRSLKRGSKPSASSASLEKRMKMWVSQSITQRFRLSRDRKVK 358
DB 299 AAASPTSSSGSSSGRTERPRSLKRGSKPSASSASLEKRMKMWVSQSITQRFRLSRDRKVK 358
QY 359 SLAVTISFGLCWAPYTLMIIRAACHGCHVDPYVYETSFLLWANSVNPVLYPLCHHS 418
DB 359 SLAVTISFGLCWAPYTLMIIRAACHGCHVDPYVYETSFLLWANSVNPVLYPLCHHS 418
QY 419 FRATFKLLCPQKIKIOPHSSLEHCWK 445
DB 419 FRATFKLLCPQKIKIOPHSSLEHCWK 445

RESULT 6

Q8WY01 PRELIMINARY; PRT; 365 AA.
AC Q8WY01;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Histamine H3 receptor isoform 2.
GN Name=HRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P.; Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor."
RL Neuropharmacology 0:0-0(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF321911; AAL71912.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.

RESULT 7

Q8WXZ9 PRELIMINARY; PRT; 373 AA.
AC Q8WXZ9;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Histamine H3 receptor isoform 4.
GN Name=HRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P.; Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor."
RL Neuropharmacology 0:0-0(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF321913; AAL71914.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR Pfam; PF00001; 7tm1; 1.

DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PRINTS; PRO1471; HISTAMINEH3R.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; 1.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR F1.2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 373 AA; 41570 MW; FA59DFC53AF4DE9 CRC64;

Query Match 81.3%; Score 1919; DB 2; Length 373;
 Best Local Similarity 82.0%; Pred. No. 1.8e-101;
 Matches 365; Conservative 0; Mismatches 0; Indels 80; Gaps 1;

QY 1 MERAPDGLNAGSALAGDAAAAGARGFSAATVLAALMALLIVATVIGNALVWLAFV 60
 DB 1 MERAPDGLNAGSALAGDAAAAGARGFSAATVLAALMALLIVATVIGNALVWLAFV 60
 QY 61 ADSSLRTQNNFLLNLAISDFLVGAFCLPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
 DB 61 ADSSLRTQNNFLLNLAISDFLVGAFCLPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
 QY 121 SAFNVLISYDRFLSVTRAVSYRAQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
 DB 121 SAFNVLISYDRFLSVTRAVSYRAQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
 QY 181 SSIPGHCYAEFFNYWYFLITASTLEFFTPFLSVTFNNLSIYLNQRTLRDLGAREAA 240
 DB 181 SSIPGHCYAEFFNYWYFLITASTLEFFTPFLSVTFNNLSIYLNQRTLRDLGAREAA 240
 QY 241 GPEPPEAQSPPPPPGCGWCKGKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV 300
 DB 241 GPEPPEAQSPPPPPGCGWCKGKGHEAMPLH- 273
 QY 301 ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMSQSFQRFELSDRDKVAKSL 360
 DB 274 -----RKVAKSL 280
 QY 361 AVISIFGLCWAPYTLMLIRAAACHGCVDPYWTYSFWLLWANSVNPVLPCHHSFR 420
 DB 281 AVISIFGLCWAPYTLMLIRAAACHGCVDPYWTYSFWLLWANSVNPVLPCHHSFR 340
 QY 421 RAFTKLLCPQKLIKIPHSSLEHCWK 445
 DB 341 RAFTKLLCPQKLIKIPHSSLEHCWK 365

RESULT 8
 Q8WY00 PRELIMINARY; PRT; 301 AA.
 AC Q8WY00;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Histamine H3 receptor isoform 3.
 GN Name=HRH3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RA Wellendorph P.; Goodman M.W.; Burstein E.S.; Nash N.R.; Brann M.R.;
 RA Weiner D.M.;
 RT "Molecular Cloning and Characterization of Functionally Distinct
 RT Isoforms of the Human Histamine H3 Receptor."
 RL Neuropharmacology 0:0-0(2002).
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF321912; AAL71913.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004969; F:histamine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.

DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PRINTS; PRO1471; HISTAMINEH3R.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; 1.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR F1.2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 301 AA; 33280 MW; EE740A2E0AB93CC9 CRC64;

Query Match 64.4%; Score 1521; DB 2; Length 301;
 Best Local Similarity 67.6%; Pred. No. 6e-79;
 Matches 301; Conservative 0; Mismatches 0; Indels 144; Gaps 1;

QY 1 MERAPDGLNAGSALAGDAAAAGARGFSAATVLAALMALLIVATVIGNALVWLAFV 60
 DB 1 MERAPDGLNAGSALAGDAAAAGARGFSAATVLAALMALLIVATVIGNALVWLAFV 60
 QY 61 ADSSLRTQNNFLLNLAISDFLVGAFCLPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
 DB 61 ADSSLRTQNNFLLNLAISDFLVGAFCLPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
 QY 121 SAFNVLISYDRFLSVTRAVSYRAQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
 DB 121 SAFNVLISYDRFLSVTRAVSYRAQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
 QY 181 SSIPGHCYAEFFNYWYFLITASTLEFFTPFLSVTFNNLSIYLNQRTLRDLGAREAA 240
 DB 181 SSIPGHCYAEFFNYWYFLITASTLEFFTPFLSVTFNNLSIYLNQRTLRDLGAREAA 240
 QY 241 GPEPPEAQSPPPPPGCGWCKGKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV 300
 DB 241 GPEPPEAQSPPPPPGCGWCKGKGHEAMPL- 272
 QY 301 ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMSQSFQRFELSDRDKVAKSL 360
 DB 273 -----
 QY 361 AVISIFGLCWAPYTLMLIRAAACHGCVDPYWTYSFWLLWANSVNPVLPCHHSFR 420
 DB 273 -----HSFR 276
 QY 421 RAFTKLLCPQKLIKIPHSSLEHCWK 445
 DB 277 RAFTKLLCPQKLIKIPHSSLEHCWK 301

RESULT 9
 Q8NI49 PRELIMINARY; PRT; 309 AA.
 AC Q8NI49;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Histamine H3 receptor isoform 6.
 GN Name=HRH3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RA Wellendorph P.; Goodman M.W.; Burstein E.S.; Nash N.R.; Brann M.R.;
 RA Weiner D.M.;
 RT "Molecular Cloning and Characterization of Functionally Distinct
 RT Isoforms of the Human Histamine H3 Receptor."
 RL Neuropharmacology 0:0-0(2002).
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF346904; AAM43829.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004969; F:histamine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO: 0007186; P-G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR003980; H3_receptor.
DR Pfam: PF00001; 7tm1; 1.
DR PRINTS; PRO0237; GPCRHHODOPS. N.
DR PRINTS; PRO1471; HISTAMINEH3.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 309 AA; 34242 MW; B7496P7D1D2A206B CRC64;

Query Match 64.4%; Score 1521; DB 2; Length 309;
Best Local Similarity 67.6%; Pred. No. 6.2e-79;
Matches 301; Conservative 0; Mismatches 0; Indels 144; Gaps 1;

QY 1 MERAPPDGLNAGSALAGDAAGGARGFSAWTAVALAALLVATVGLNALVMAFV 60
DB 1 MERAPPDGLNAGSALAGDAAGGARGFSAWTAVALAALLVATVGLNALVMAFV 60
QY 61 ADSSLRQNNFLLNLAIISDFLVGAFCLPYVYVLTGRWTFGRGLCKLWLVVDVLLCTS 120
DB 61 ADSSLRQNNFLLNLAIISDFLVGAFCLPYVYVLTGRWTFGRGLCKLWLVVDVLLCTS 120
QY 121 SAFNVLISYDFLSVTRAVSRAOQDTRRAVRKMLLVWVLAFLLYGPAILSWELSGG 180
DB 121 SAFNVLISYDFLSVTRAVSRAOQDTRRAVRKMLLVWVLAFLLYGPAILSWELSGG 180
QY 181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNITQRTLRDLGAREAA 240
DB 181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNITQRTLRDLGAREAA 240
QY 241 GPEPPEAQSPPPPGCWGCKGHEAMPVLRHYGVGEAAGVAGAGATLGGGGGGGSV 300
DB 241 GPEPPEAQSPPPPGCWGCKGHEAMPVLRHYGVGEAAGVAGAGATLGGGGGGGSV 300
QY 301 ASPTSSSGSSRGTERPSLRKSGKSPASSASLEKRMKMWVSQSFQRTLRSLDRKVAKSL 360
DB 273 ----- 272
QY 361 AVIVSIFGLCWAPYTLMLIIRAACHGCHVDPYVWYTSFWLLWANSVNPVLYPLCHHFR 420
DB 273 -----HSFR 276
QY 421 RAFTKLLCPQKLIQPHSSLEHCWK 445
DB 277 RAFTKLLCPQKLIQPHSSLEHCWK 301

RESULT 10
Q8K116 ID Q8K116 PRELIMINARY; PRT; 247 AA.
AC Q8K116
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Hrh3 protein (Fragment).
GN Name=Hrh3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zdobych B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028947; AAH28947.1; -;
DR MGI; MGI:2139279; Hrh3.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR003980; H3_receptor.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PRO0237; GPCRHHODOPS. N.
DR PRINTS; PRO1471; HISTAMINEH3.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR_F1_2; 1.
FT NON_TER 1
SQ SEQUENCE 247 AA; 26937 MW; D0154BD9995A01B1 CRC64;

Query Match 51.8%; Score 1223; DB 2; Length 247;
Best Local Similarity 91.5%; Pred. No. 4.2e-62;
Matches 227; Conservative 6; Mismatches 13; Indels 2; Gaps 2;

QY 199 LITASTLEFFTPFLSVTFNLSIYLNITQRTLRDLGAREAAAGPEPPEAOPSPPPP-PG 257
DB 1 LITASTLEFFTPFLSVTFNLSIYLNITQRTLRDLGAREAAAGPEPPEAOPSPPPP-PG 257
QY 258 CWGQKQKCHGAMPVLRHYGVGEAAGVAGAGATLGGGGGGSVASPTSSSGSSRGTERP 317
DB 60 CWGQKQKCHGAMPVLRHYGVGEAAGVAGAGATLGGGGGGSVASPTSSSGSSRGTERP 119
QY 318 RSLKRGSKSPASSASLEKRMKMWVSQSFQRTLRSLDRKVAKSLAVIVSIFGLCWAPYTL 377
DB 120 RSLKRGSKSPASSASLEKRMKMWVSQSFQRTLRSLDRKVAKSLAVIVSIFGLCWAPYTL 179
QY 378 MIIRAACHGCHVDPYVWYTSFWLLWANSVNPVLYPLCHHFRRAFTKLLCPQKLIQPH 437
DB 180 MIIRAACHGCHVDPYVWYTSFWLLWANSVNPVLYPLCHHFRRAFTKLLCPQKLIQPH 239
QY - 438 SLEHCWK 445
DB 240 GSLEHCWK 247

RESULT 11
Q8ZM33 ID Q8ZM33 PRELIMINARY; PRT; 473 AA.
AC Q8ZM33
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE SI-bz34G2.4 (Novel protein similar to human histamine receptor H3 (HRH3)).
DE (HRH3).
GN Name=si:rp71-34g2.4; Synonyms=SI-bz34G2.4;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Tracey A.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AL928906; CAE49238.1; -.
DR ZFIN; ZDB-GENE-040724-204; si:tp71-34g2.4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0004872; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.; IEA.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1_receptor.
DR PRINTS; PR00237; GFCRRHODPSN.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 473 AA; 53506 MW; 032FEC7C2D8C5E57 CRC64;

Query Match 50.2%; Score 1186; DB 2; Length 473;
Best Local Similarity 54.2%; Pred. No. 9.5e-60;
Matches 240; Conservative 51; Mismatches 86; Indels 66; Gaps 8;

QY 29 FSAWTAVALAAALMALIVATLVGNALVMAFAVDSSLTQNFPLNLAIASDFLVGAFCI 88
DB 59 FSPSTSFITVLMTLLVFATVIGNALVILAFVVEKSLRTQGNFFPLNLAIADFLVGFCI 118
QY 89 PLVPVPLTGRVTFRGCLCKMLWDVLYLLCTSSAFNIVLISYDRFLSVTRAVSYRAOQGD 148
DB 119 PVVIPVLIGEWRLGRLCKMLWDVLMCTASVENIVLSIFDRFSQVTKAVSRCQGI 178
QY 149 TRRAVRKMLLVMLAPFLGYPAILLSWEYLSCGSSIPGECHYAEPFYNNYFLITASTLEFF 208
DB 179 TKDAVLKLCVLAAPFLLYGPAIIISWEHTGGVVDPDGCEYAEFPYNNYFLWTASTVEFF 238
QY 209 TPPLSVTFNLSIYNIQRTLRDLGAREAGPEPPPEAOPS-----PPPPPCGW 259
DB 239 TPFISVTYFNLSIYNIRNCAMR-----EQFTYVRLRSFKPKP----- 278
QY 260 GCWKQGHEAM-----PLHYGVGEAAVGAEGEATLGCGGGGSVASPTSSSGSSSRG 313
DB 279 ----LGAGDVQVFFVRPVESERVADLASRKCCRL-----ASTAKVSAAFNGRQ 326
QY 314 TERPSLRKSGKP-----SASSASL-----EKRMKVVSOFTRFLRSRDVK 355
DB 327 SKERDSTLADLPLOQEERILAASEAQPHYVDHSAGPHHRPDWA-SLANRFELSRDKK 395
QY 356 VAKSLAVVISIFGLCWAPTLLMITRAACHGHCVPDYWYTSFWLLWANSVNPVLPLC 415
DB 386 VAKSLAVIVCFGLCWAPTLLMITRAACHGCQVQHYLYEIFSWLLWNINSINILYPLC 445
QY 416 HHSFRAPFTKLCPQKLIKOPHS 438
DB 446 HSFKRFRSKLKCPKTYKIQQN 468

RESULT 12
QBNC4 ID QBNC4 PRELIMINARY; PRT; 210 AA.

AC QBNC4; DB 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90249.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Neuropharmacology 0:0-0(2002)
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF346903; AAM43828.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.; IEA.
DR InterPro; IPR000276; GPCR Rhodpsn.

Masuhio Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK074730; BAC11167.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004969; F:histamine receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.; IEA.
InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm_1; 1_receptor.
PRINTS; PR00237; GFCRRHODPSN.
PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
SQ SEQUENCE 210 AA; 24046 MW; 952F3FFED60077CAD CRC64;

Query Match 48.2%; Score 1137; DB 2; Length 210;
Best Local Similarity 72.4%; Pred. No. 2.8e-57;
Matches 210; Conservative 0; Mismatches 0; Indels 80; Gaps 1;

QY 156 MLVWVLAFLYGPAILLSWEYLSCGSSIPGECHYAEPFYNNYFLITASTLEFFTPFLSVT 215
DB 1 MLVWVLAFLYGPAILLSWEYLSCGSSIPGECHYAEPFYNNYFLITASTLEFFTPFLSVT 60
QY 216 FFNLSIYNIQRTLRDLGAREAGPEPPPEAOPSPPPGCWGQKGHGGEAMPLHRY 275
DB 61 FFNLSIYNIQRTLRDLGAREAGPEPPPEAOPSPPPGCWGQKGHGGEAMPLH-- 118
QY 276 VGGEAAVGAEGEATLGCGGGGSVASPTSSSGSSRGTERRSLKRGSKPSASSASLEK 335
DB 119 ----- 118
QY 336 RMKMVSQSOTQRFRLSDRVKAVSLAVISIFGLCWAPTLLMITRAACHGHCVPDYWYE 395
DB 119 -----RKVAKSLAVISIFGLCWAPTLLMITRAACHGHCVPDYWYE 160
QY 396 TSFWLLWANSVNPVLPLCHSPRRAPFTKLCPQKLIKOPHSLEHCWK 445
DB 161 TSFWLLWANSVNPVLPLCHSPRRAPFTKLCPQKLIKOPHSLEHCWK 210

RESULT 13
QBNS10 ID QBNS10 PRELIMINARY; PRT; 200 AA.

AC QBNS10; DB 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Histamine H3 receptor isoform 5.
GN Name=HRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Neuropharmacology 0:0-0(2002)
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF346903; AAM43828.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.; IEA.
DR InterPro; IPR000276; GPCR Rhodpsn.

DR InterPro; IPR003980; H3 receptor.
DR Pfam; PF00001; 7tm 1; 1_1-
DR PRINTS; PRO0237; GPCRHHODPSN.
DR PRINTS; PRO1471; HISTAMINEH3R.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 200 AA; 21612 MW; 2038D14BC186D1EA CRC64;

Query Match 36.4%; Score 860; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPPDGLNAGSALAGDAARAGARGSAWTAVALAALMALLIVATVIGNALVMAFV 60
DB 1 MERAPPDGLNAGSALAGDAARAGARGSAWTAVALAALMALLIVATVIGNALVMAFV 60

QY 61 ADSSLRQNNFLLNLAIISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDVLLCTS 120
DB 61 ADSSLRQNNFLLNLAIISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDVLLCTS 120

QY 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMVLVWVLAFLLYGPA 170
DB 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMVLVWVLAFLLYGPA 170

RESULT 14
Q865E3 PRELIMINARY; PRT; 147 AA.
ID Q865E3
AC Q865E3
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE Histamine receptor H3 (fragment).
GN Name=HRH3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Witte D.G., Ebershade T.A., Hancock A.A., Yao B.B.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AY231165; AAO63755.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR InterPro; IPR0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1_1-
DR PRINTS; PRO0237; GPCRHHODPSN.
DR PRINTS; PRO1471; HISTAMINEH3R.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 147
SQ SEQUENCE 147 AA; 16900 MW; 67F6A741B518B54E CRC64;

Query Match 31.9%; Score 754; DB 2; Length 147;
Best Local Similarity 95.9%; Pred. No. 1.2e-35;
Matches 141; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 72 FLNLAIISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDVLLCTSSAFNIVLISYD 131
DB 1 FLNLAIISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDVLLCTSSAFNIVLISYD 60

QY 132 RFLSVTRAVSYRAQQGDTTRAVRKMVLVWVLAFLLYGPAISWELSGGSSIPEGHCAE 191
DB 132 RFLSVTRAVSYRAQQGDTTRAVRKMVLVWVLAFLLYGPAISWELSGGSSIPEGHCAE 191

DB 61 RFLSVTRAVSYRAQQGDTTRAVRKMVLVWVLAFLLYGPAISWELSGGSSIPEGHCAE 120
QY 192 FFYNNWFLITASTLEFFTPFLSVTFEN 218
DB 121 FFYNNWFLITASTLEFFTPFLSVTFEN 147

RESULT 15
HH4R_HUMAN STANDARD; PRT; 390 AA.
ID HH4R_HUMAN
AC Q9H3N8; Q9GZ00;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Histamine H4 receptor (HH4R) (GPRV53) (G protein-coupled receptor 105)
DE (GPCR105) (SP9105) (AXOR35).
GN Name=HRH4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20538417; PubMed=10973974; DOI=10.1074/jbc.M006480200;
ODA T., Morikawa N., Saito Y., Masuho Y., Matsumoto S.-I.;
RT "Molecular cloning and characterization of a novel type of histamine receptor preferentially expressed in leukocytes";
RL J. Biol. Chem. 275:36781-36786(2000).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Leukocyte;
RX MEDLINE=20568725; PubMed=11118334; DOI=10.1006/bbrc.2000.4008;
RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
RT "Molecular cloning and characterization of a new human histamine receptor, HH4R";
RL Biochem. Biophys. Res. Commun. 279:615-620(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Jones P.G., Wu S., Betty M.;
RT "Cloning of a novel histamine receptor";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Bone marrow;
RX PubMed=11179434;
RA Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofstra C.L., Blevitt J.,
PY Pyati J., Li X., Chai W., Carruthers N., Lovenberg T.W.;
RT "Cloning and pharmacological characterization of a fourth histamine receptor (H4) expressed in bone marrow";
RL Mol. Pharmacol. 59:420-426(2001).
RN [5]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Eosinophil;
RX MEDLINE=21104636; PubMed=11181941;
RA Morse K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A.,
RA Anthes J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N.,
RA Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M.,
RA Monsma F.J. Jr.;
RT "Cloning and characterization of a novel human histamine receptor";
RL J. Pharmacol. Exp. Ther. 296:1058-1066(2001).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=21106320; PubMed=11179436;
RA Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan I.J.,
RA Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L.,
RA Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S.,
RA Bergsma D.J., Fitzgerald L.R.;
RT "Cloning, expression, and pharmacological characterization of a novel human histamine receptor";
RL Mol. Pharmacol. 59:434-441(2001).
RN [7]
RP SEQUENCE FROM N.A.
RA O'Reilly M.A.;

"Identification of a histamine H4 receptor on human eosinophils - Role in eosinophil chemotaxis.";
 Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

SEQUENCE FROM N.A.

Puhl H.L. III, Ikeda S.R., Aronstam R.S.;

"cDNA clones of human proteins involved in signal transduction

sequenced by the Guthrie cDNA resource center (www.cdna.org).";

Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

CC !- FUNCTION: The H4 subclass of histamine receptors could mediate the histamine signals in peripheral tissues. Displays a significant level of constitutive activity (spontaneous activity in the absence of agonist).

CC !- SUBCELLULAR LOCATION: Integral membrane protein.

CC !- TISSUE SPECIFICITY: Expressed primarily in the bone marrow and eosinophils. Shows preferential distribution in cells of

immunological relevance such as T-cells, dendritic cells, monocytes, mast cells, neutrophils. Also expressed in a wide

variety of peripheral tissues, including the heart, kidney, liver, lung, pancreas, skeletal muscle, prostate, small intestine,

spleen, fetal liver and lymph node.

CC !- INDUCTION: Expression is either up-regulated or down-regulated upon activation of the lymphoid tissues and this regulation may depend on the presence of IL-10 or IL-13.

CC !- MISCELLANEOUS: Does not bind diphenhydramine, loratadine, ranitidine, cimetidine and chlorpheniramine. Shows modest affinity for dimaprit, imipramine, clobenpropit, thioperamide, burinamide

clobazepam, imiprep and imetit. The order of inhibitory activity was imetit > clobenpropit > burinamide > thioperamide.

CC Clobenpropit behaves as a partial agonist, dimaprit and imipramine show some agonist activity while clobazepam behaves as a full agonist. Thioperamide shows inverse agonism (enhances CAMP activity). The order of inhibitory activity of histamine derivatives was Histamine > N-alpha-methylhistamine > R(-)-alpha-methylhistamine > S(+)-alpha-methylhistamine. Both N-alpha-methylhistamine > R(-)-alpha-methylhistamine behave as full agonists.

CC !- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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DR EMBL; AB044934; BAB13698.1; -
 DR EMBL; AB045370; BAB20091.1; -
 DR EMBL; AF307973; AAG32052.1; -
 DR EMBL; AF312230; AAK12081.1; -
 DR EMBL; AF329449; AAK33542.1; -
 DR EMBL; AF325356; AAL01684.1; -
 DR EMBL; AJ298292; CAC83493.1; -
 DR EMBL; AY136745; AAN01271.1; -
 DR PIR; JC7566; JC7566.
 DR Genew; HGNC:17383; HRH4.
 DR MIM; 606792; -
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0004969; F:histamine receptor activity; NAS.
 DR InterPro; IPR00276; GPCR Rhodpsn.
 DR InterPro; IPR008102; Histamine_recept_H4.
 DR Pfam; PF00001; 7tm 1; 1
 DR PRINTS; PR00237; GPCRHOOPSN.
 DR PRINTS; PR01726; HISTAMINEH4R.
 DR PROSITE; PS00237; G.PROTEIN RECEPTOR F1.1; 1.
 DR PROSITE; PS0262; G.PROTEIN RECEPTOR F1.2; 1.
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KW Transmembrane.

FT DOMAIN 1 19 Extracellular (Potential).

FT TRANSMEM 20 40 1 (Potential).

FT DOMAIN 41 52 Cytoplasmic (Potential).

FT TRANSMEM 53 73 2 (Potential).

FT DOMAIN 74 87 Extracellular (Potential).
 FT TRANSMEM 88 108 3 (Potential).
 FT DOMAIN 109 131 Cytoplasmic (Potential).
 FT TRANSMEM 132 152 4 (Potential).
 FT DOMAIN 153 172 Extracellular (Potential).
 FT TRANSMEM 173 193 5 (Potential).
 FT DOMAIN 194 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 325 6 (Potential).
 FT DOMAIN 326 341 Extracellular (Potential).
 FT TRANSMEM 342 362 7 (Potential).
 FT DOMAIN 363 390 Cytoplasmic (Potential).
 FT DISULFID 5 5 By similarity.
 FT CARBOHYD 8 164 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 9 9 N-linked (GlcNAc...) (Potential).
 FT LIPID 374 374 S-palmitoyl cysteine (Potential).
 FT CONFLICT 138 138 A -> V (in Ref. 1).
 FT CONFLICT 206 206 H -> R (in Ref. 1).
 FT CONFLICT 253 253 Q -> R (in Ref. 1).
 SQ SEQUENCE 390 AA; 44495 MW; C986B8AB7FF912C3 CRC64;

Query Match 30.7%; Score 724; DB 1; Length 390;

Best Local Similarity 38.6%; Pred. No. 1.4e-33;

Matches 164; Conservative 56; Mismatches 131; Indels 74; Gaps 10;

QY 30 SAAMTAVLAALMALIVATVIGNALVMLAFVADSSLRQTNNFFLNLAISDFLVGAFCIP 89

Db 11 SLSTRVTLAFFMSLVAFALMGLNALVILAFVVDKMLHRSSVFFLNLAISDFLVGVISIP 70

QY 90 LYVPVLTGRWTFGRGLKLVVDYLLCTSAFNVLISYDRFLSVTVAVSYRAQQGT 149

Db 71 LYIPTHLP-EDWDFGKEICVFWLTDTLLCTASVYVNLISYDRFLSVTVAVSYRTOHTGV 129

QY 150 RRAVRKMLLVVLAFLYGPAIL---SWEYLSGGSSIPG-HCYAEFFVNWYFLITASTL 205

Db 130 LKIVTLVAVVWVLAFLVNGPMLVSEWK-----DEGSECEGPFSEWILAITSL 181

QY 206 EFTFPFLSVTFNLSIYLNIIQRTLRDLRGAREAGPEPPPEAQPSPPPPPCGWCQKG 265

Db 182 EFVIPVLVAVFNMNIY-----WSLWKRD 205

QY 266 HGEAMPLHYGVGEAAVCAEAGEATLGGGGGGSVASTSSGSS-----SRGTERPR 318

Db 206 HLSRCQSH-----PGLTAVSSNICGHSFGRLLSSRRSLASASTEVPAFPHSERQRRKS 257

QY 319 SLKRGSKPSASSASILEKRMKVSQSFT-----QRFRLSRDRKVAKSLAVIVSIIFGLCWA 372

Db 258 SLMTSSRTYMTNSNTIASKMGSGFSQSDSVALHQREHVELLRARLRKLSLAILLGVFAVCWA 317

QY 373 PYTLMIITRAACHGHCVP-DYWTYSFWLLWANSVNPVLYPLCHHSFRRFAFTKLLCPQK 431

Db 318 PYSLFTVILSVSSATGPKSVWYRIAFWLQWFNSFVNPLLYPLCHKRFQKAFKIFC--- 374

QY 432 LKIQP 436

Db 375 IKKQP 379

Search completed: June 2, 2005, 20:40:46

Job time : 87 secs

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 05:14:06 ; Search time 445.596 Seconds
(without alignments)
9911.021 Million cell updates/sec

Title: US-10-727-021-5
Perfect score: 2699
Sequence: 1 ccacggtccggtcgga.....aaaaaaaaaaaaaaaaaaaaa 2699

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2699	100.0	2699	3	US-09-167-354-5
2	2699	100.0	2699	3	US-09-642-855-8
3	2699	100.0	2699	3	US-09-642-514-5
4	2635.2	97.6	2689	2	US-08-985-090-1
5	2635.2	97.6	2689	3	US-09-165-543-1
6	2633.6	97.6	2665	4	US-09-949-016-5059
7	1947.8	72.2	9293	4	US-09-949-016-16801
8	1590.2	58.9	1893	4	US-09-891-053-13
9	1384.8	51.3	3244	3	US-09-165-543-4
10	1360.4	50.4	2050	4	US-09-891-053-21
11	1335	49.5	1335	3	US-09-167-354-6
12	1335	49.5	1335	3	US-09-642-855-6
13	1335	49.5	1335	3	US-09-642-514-6
14	1331.8	49.3	1335	2	US-08-985-090-3
15	1331.8	49.3	1335	3	US-09-165-543-3
16	1208	44.8	2700	4	US-09-891-053-5
17	1201.8	44.5	1953	4	US-09-891-053-26
18	1072.2	39.7	1338	3	US-09-165-543-6
19	1032.6	38.3	2218	2	US-08-985-090-4
20	1032.6	38.3	2218	3	US-09-165-543-31
21	899.2	33.3	1239	4	US-09-891-053-2
22	852.2	31.6	1086	2	US-08-985-090-6
23	852.2	31.6	1086	3	US-09-165-543-33
24	750.8	27.8	1056	3	US-09-524-162-1
25	600.6	22.3	601	4	US-09-949-016-177027
26	525.4	19.5	1350	4	US-09-891-053-11
27	375	13.9	375	3	US-09-167-354-8

c 25 600.6 22.3 601 4 US-09-949-016-177027

26 525.4 19.5 1350 4 US-09-891-053-11

27 375 13.9 375 3 US-09-167-354-8

28 375 13.9 375 3 US-09-642-855-8 Sequence 8, Appli
29 375 13.9 375 3 US-09-642-514-8 Sequence 8, Appli
30 177.4 6.6 3604 4 US-09-016-434-1180 Sequence 1180, Ap
31 175.2 6.5 1956 1 US-08-313-553-6 Sequence 6, Appli
32 175.2 6.5 1956 3 US-08-767-993-6 Sequence 6, Appli
33 175 6.5 2595 4 US-09-016-434-1178 Sequence 1178, Ap
34 173.6 6.4 1440 4 US-09-826-509-518 Sequence 518, App
35 173.4 6.4 448 4 US-09-891-053-12 Sequence 12, Appli
36 173.2 6.4 1422 4 US-09-826-509-512 Sequence 512, App
37 172.4 6.4 1581 1 US-08-313-553-8 Sequence 8, Appli
38 172.4 6.4 1581 3 US-08-767-993-8 Sequence 8, Appli
39 171.6 6.4 1386 4 US-09-016-434-1339 Sequence 1339, Ap
40 162.6 6.0 1382 4 US-09-016-434-1256 Sequence 1256, Ap
41 155.6 5.8 1599 4 US-09-826-509-520 Sequence 520, App
42 155.6 5.8 2261 4 US-09-016-434-1176 Sequence 1176, Ap
43 143.2 5.3 1845 4 US-09-614-034-188 Sequence 188, App
44 138.6 5.1 4401 4 US-09-614-034-192 Sequence 192, App
45 131 4.9 1344 4 US-09-825-923-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-167-354-5
; Sequence 5, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-5

Query Match 100.0%; Score 2699; DB 3; Length 2699;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACGCTCCGCGCTGCACGGTCCGACCGGCTCAGGCTCCGGCTCCTCTCCC 60
DB 1 CCACGCTCCGCGCTGCACGGTCCGACCGGCTCAGGCTCCGGCTCCTCTCCC 60
QY 61 GCTGACGACGCGCTGCACCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCA 120
DB 61 GCTGACGACGCGCTGCACCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCA 120
QY 121 CGGCTGTCTGTGGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGGAA 180
DB 121 CGGCTGTCTGTGGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGGAA 180
QY 181 ACCGACCGCGCAAGGCGCCCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 181 ACCGACCGCGCAAGGCGCCCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 241 CCAGCTCTCGGCGCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 241 CCAGCTCTCGGCGCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 GGAGCG 360

QY 2521 CAAGGGCTGCAGGGGGCTCCAGAGAGGTGCCCGGGGAGGGGCGCTTCGCCATGTGCT 2580
Db 2521 CAAGGGCTGCAGGGGGCTCCAGAGAGGTGCCCGGGGAGGGGCGCTTCGCCATGTGCT 2580
QY 2581 GTGCAACCGTGCACCGCGCTCTGCATGCTCTCTGCTGTCGCCGCTGCCCTTCA 2640
Db 2581 GTGCAACCGTGCACCGCGCTCTGCATGCTCTCTGCTGTCGCCGCTGCCCTTCA 2640
QY 2641 AACCGTGAGGTCAACATTAAGTGTATTTTAAAAAAGGGGGGGGGGGGGGGGGGG 2699
Db 2641 AACCGTGAGGTCAACATTAAGTGTATTTTAAAAAAGGGGGGGGGGGGGGGGGGG 2699

RESULT 2

US-09-642-855-5
; Sequence 5, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Brandler, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JWV
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-5

Query Match 100.0%; Score 2699; DB 3; Length 2699;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2699; Conservative 0;
QY 1 CCACGCGTCCGCGGCTGCACGGTCCGACCGGAGCGGCTCAGGCTCCGGCTCTCTCC 60
Db 1 CCACGCGTCCGCGGCTGCACGGTCCGACCGGAGCGGCTCAGGCTCCGGCTCTCTCC 60
QY 61 GTGCAAGCGCGCGTGCAGCGGCTCCGCGGCTCCGCGGCTCCGCGGCTCCGCGG 120
Db 61 GTGCAAGCGCGCGTGCAGCGGCTCCGCGGCTCCGCGGCTCCGCGGCTCCGCGG 120
QY 121 CGCGCTGTCTGGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 121 CGCGCTGTCTGGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 ACCGACCGCGCAAGGGCGCGCAAGAGAGAGGCTCCCGGGCGGGGGCGCGCGCG 240
Db 181 ACCGACCGCGCAAGGGCGCGCAAGAGAGAGGCTCCCGGGCGGGGGCGCGCGCG 240
QY 241 CCCAGCTCTCG 300
Db 241 CCCAGCTCTCG 300
QY 301 GGAGCG 360
Db 301 GGAGCG 360
QY 361 GCG 420
Db 361 GCG 420
QY 421 GCGCGTGTCTAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480

Db 421 GCGCGTGTCTAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 481 CGACTCGAGCGCTCCGCAACCCAGAAACAATTTCTTCTGTCTCAACCTCGCCATCTCCGACTT 540
Db 481 CGACTCGAGCGCTCCGCAACCCAGAAACAATTTCTTCTGTCTCAACCTCGCCATCTCCGACTT 540
QY 541 CTTGTCGGCGCTTCTGATCCCACTGTATGTACCTTACCTGCTGACAGGCGCGTGGAC 600
Db 541 CTTGTCGGCGCTTCTGATCCCACTGTATGTACCTTACCTGCTGACAGGCGCGTGGAC 600
QY 601 CTTGSGCGCGGCGCTTCTGCAAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db 601 CTTGSGCGCGGCGCTTCTGCAAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGT 660
QY 661 TGCCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGCTCGGTCAACCGAGCGTCTC 720
Db 661 TGCCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGCTCGGTCAACCGAGCGTCTC 720
QY 721 ATACCGGCGCGAGCGGTGACACCGCGCGGCGGAGTGGGAGAGATGCTGCTGTGTGTGT 780
Db 721 ATACCGGCGCGAGCGGTGACACCGCGCGGCGGAGTGGGAGAGATGCTGCTGTGTGTGT 780
QY 781 GCTGSCCTTCTGCTGTACGAGCAGCCATCTGAGCTGGGAGTACCTGCTCGGGGCGAG 840
Db 781 GCTGSCCTTCTGCTGTACGAGCAGCCATCTGAGCTGGGAGTACCTGCTCGGGGCGAG 840
QY 841 CTCCATCCCGAGGCGGCTGCTATGCGAGTCTTCTTACACTGCTTCTTCTTCTTCTTCT 900
Db 841 CTCCATCCCGAGGCGGCTGCTATGCGAGTCTTCTTACACTGCTTCTTCTTCTTCTTCT 900
QY 901 GGTCTTCAACCTGAGGTTCTTTCACCGCTTCTTACCGCTTCTTCTTCTTCTTCTTCT 960
Db 901 GGTCTTCAACCTGAGGTTCTTTCACCGCTTCTTACCGCTTCTTCTTCTTCTTCTTCT 960
QY 961 CTACTGAACTCCAGAGCGCGCGCGCTCCGCTGCTGGTGGGCTCGAGAGCGAGCGG 1020
Db 961 CTACTGAACTCCAGAGCGCGCGCGCTCCGCTGCTGGTGGGCTCGAGAGCGAGCGG 1020
QY 1021 CCCCAGGCGCGCTCCGAGGCGCGCGCTTCAACCGCGCGCGCTGCTGCTGCGGCTG 1080
Db 1021 CCCCAGGCGCGCTCCGAGGCGCGCGCTTCAACCGCGCGCGCTGCTGCTGCGGCTG 1080
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Db 1081 CTGGCAGAGGCG 1140
QY 1141 GGTAGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
Db 1141 GGTAGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 1201 TTTACCCACCTCCAGCTCCGCGCGCTTCTCGAGGCGCGCTGAGAGCGCGCGCTCACTCAA 1260
Db 1201 TTTACCCACCTCCAGCTCCGCGCGCTTCTCGAGGCGCGCTGAGAGCGCGCGCTCACTCAA 1260
QY 1261 GAGGGGCTCAAGCGCTCGCGCTTCTCGCGCTTCTCGAGAGCGCGCATGAAGTGTGTGTC 1320
Db 1261 GAGGGGCTCAAGCGCTCGCGCTTCTCGCGCTTCTCGAGAGCGCGCATGAAGTGTGTGTC 1320
QY 1321 CCAGAGCTTCAACCGCGCTTCTCGCGCTTCTCGAGAGCGCGCATGAAGTGTGTGTC 1380
Db 1321 CCAGAGCTTCAACCGCGCTTCTCGCGCTTCTCGAGAGCGCGCATGAAGTGTGTGTC 1380
QY 1381 CGTCACTGTGAGCATCTTTTGGGCTTCTGCTGGGCGCGCATGAGTGTGTGTGTGTGTGT 1440
Db 1381 CGTCACTGTGAGCATCTTTTGGGCTTCTGCTGGGCGCGCATGAGTGTGTGTGTGTGT 1440
QY 1441 GCGCGCTTCCATGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Db 1441 GCGCGCTTCCATGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 GTGGGCGCAACTCGGCTGTCAACCTTCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
Db 1501 GTGGGCGCAACTCGGCTGTCAACCTTCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1560

QY 1561 GGCCTTCAACAGCTGCTCTGCCCCCAGAGCTCAAAATCCAGCCCCCAGCTCCCTGGA 1620
DB 1561 GGCCTTCAACAGCTGCTCTGCCCCCAGAGCTCAAAATCCAGCCCCCAGCTCCCTGGA 1620
QY 1621 GCACGTCTGGAAGTGAAGTGGCCACACAGAGCTCCCTCAGCCACGCTCTCTCAGCCCCAG 1680
DB 1621 GCACGTCTGGAAGTGAAGTGGCCACACAGAGCTCCCTCAGCCACGCTCTCTCAGCCCCAG 1680
QY 1681 GTCTCTGGGCATCTGGGCCCTGCTGCCCCCTACCCGGCTCGTTCGCCAGGGGTGAGCCC 1740
DB 1681 GTCTCTGGGCATCTGGGCCCTGCTGCCCCCTACCCGGCTCGTTCGCCAGGGGTGAGCCC 1740
QY 1741 GCGCTGTCTGGGCCCTCTTAATGCCACGGAGCCACCTGCGCATGGAGGCCCTTC 1800
DB 1741 GCGCTGTCTGGGCCCTCTTAATGCCACGGAGCCACCTGCGCATGGAGGCCCTTC 1800
QY 1801 CTGGGTGGCCAGAGGGCCCTCACTGGCTGAGCTGGAGCTGGGTGGCGGCCCTGGCC 1860
DB 1801 CTGGGTGGCCAGAGGGCCCTCACTGGCTGAGCTGGAGCTGGGTGGCGGCCCTGGCC 1860
QY 1861 CCCAATTCTGCTCCACCGGGAGGACAGTCTGGAGTCCACACATGCTGCCACCC 1920
DB 1861 CCCAATTCTGCTCCACCGGGAGGACAGTCTGGAGTCCACACATGCTGCCACCC 1920
QY 1921 CCGTGTGGTCCACCGCTTCGAGTTACTGGTTGGTGTCTTCCAAAGCAGCACTGG 1980
DB 1921 CCGTGTGGTCCACCGCTTCGAGTTACTGGTTGGTGTCTTCCAAAGCAGCACTGG 1980
QY 1981 GTGTGCTCAGAGCTTCCTGCCCTAGCAGTTTCCTCTGACGTGACACACCTGACACCC 2040
DB 1981 GTGTGCTCAGAGCTTCCTGCCCTAGCAGTTTCCTCTGACGTGACACACCTGACACCC 2040
QY 2041 CTTGACACACCTGACACCGTCTCTCCCGGCAAGCCAGACACTGCTTTGCTG 2100
DB 2041 CTTGACACACCTGACACCGTCTCTCCCGGCAAGCCAGACACTGCTTTGCTG 2100
QY 2101 CTTTCTGTCTCTGATTAAGCTCTAGGCTGAGCTGAGCTTTCACCCCTCTTCCACCACTCT 2160
DB 2101 CTTTCTGTCTCTGATTAAGCTCTAGGCTGAGCTGAGCTTTCACCCCTCTTCCACCACTCT 2160
QY 2161 CTCTGCCCCAAAGTGTCAAGGGGCCCTAGGAACTCTGAAGCTGTCTCTGCTTTTCA 2220
DB 2161 CTCTGCCCCAAAGTGTCAAGGGGCCCTAGGAACTCTGAAGCTGTCTCTGCTTTTCA 2220
QY 2221 TTCTGGGTGTTTTCAGAAAGATGAAGAAACATGTCTGAACTTTGATTTCTGGG 2280
DB 2221 TTCTGGGTGTTTTCAGAAAGATGAAGAAACATGTCTGAACTTTGATTTCTGGG 2280
QY 2281 ATGTTTAATCAAGAGAGACAAATTTGCTGAGAGCTCAGGGTGGATTGGCAGGTGGG 2340
DB 2281 ATGTTTAATCAAGAGAGACAAATTTGCTGAGAGCTCAGGGTGGATTGGCAGGTGGG 2340
QY 2341 CTCCACAGCCCTCTCTCCCTAAGCTTCCGGCTGAGCTGCGAGCTGCTTTCTGCC 2400
DB 2341 CTCCACAGCCCTCTCTCCCTAAGCTTCCGGCTGAGCTGCGAGCTGCTTTCTGCC 2400
QY 2401 CACCCCGCTCTGGGCTCAACACAGCCCTGGTGGCCAAAGCCTGCCCGGCCACTCTGTTT 2460
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QY 2461 GCTACCCAGGACCTCTGGGGTGTGGAGAGAGGGGCCCGGCTGGGCCCGAGGGTCC 2520
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DB 2521 CAAGCGCTGACGGGGCTCAGAGAGAGTGGCCCGGAGGGGGCGCTTCGCAATGTGCT 2580
QY 2581 GTGCAACCGGTGCAACCGCTCTGCAATGCTCTCTGCTGTGCGCGCTGCGCTGCCA 2640
DB 2581 GTGCAACCGGTGCAACCGCTCTGCAATGCTCTCTGCTGTGCGCGCTGCGCTGCCA 2640

QY 2641 AACCGTGAAGTCAAAATAAGTGATTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA 2699
DB 2641 AACCGTGAAGTCAAAATAAGTGATTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA 2699
RESULT 3
US-09-642-514-5
; Sequence 5, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Javaahree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-514-5
Query Match 100.0%; Score 2699; DB 3; Length 2699;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACGCGTCCGCGGCTGCACGCTCGACCGGACCGGACGCGCTCAGGCTCCGGTCTCTCTCC 60
DB 1 CCACGCGTCCGCGGCTGCACGCTCGACCGGACCGGACGCGCTCAGGCTCCGGTCTCTCTCC 60
QY 61 GCTGACAGCAGCGGCTGCGGCCCTCCGCGCTCGGATCCGCGCCCGGCGCCCTCCGCGCA 120
DB 61 GCTGACAGCAGCGGCTGCGGCCCTCCGCGCTCGGATCCGCGCCCGGCGCCCTCCGCGCA 120
QY 121 CGCGTGTCTGCGGCCCGGCGCCCGGCGCGGACCATGCGCTGGGCGGCCCGCCAGGGA 180
DB 121 CGCGTGTCTGCGGCCCGGCGCCCGGCGCGGACCATGCGCTGGGCGGCCCGCCAGGGA 180
QY 181 ACCGACCCGCGCAAGGCGCCGCAAGACGAGGCTCCCGGCGCGGCGCCCTCCCGCGCG 240
DB 181 ACCGACCCGCGCAAGGCGCCGCAAGACGAGGCTCCCGGCGCGGCGCCCTCCCGCGCG 240
QY 241 CCCAGCTCTCGGCGCGGCGCCCTGCGCCCGCGCTCCGAGCCGCGTGAAGCTGCGGGCCAT 300
DB 241 CCCAGCTCTCGGCGCGGCGCCCTGCGCCCGCGCTCCGAGCCGCGTGAAGCTGCGGGCCAT 300
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DB 301 GGAGGCGCGCGCGCGCGCGCGCTGAAACGCTTCGGGGGGCGCTGGGGGGGATGCGCG 360
QY 361 GGCGGCGCGCGGGCGCGCGCTTCTCGGCGAGCCCTGAGACCGCGGTGCTGGCGCGCTCAT 420
DB 361 GGCGGCGCGGGCGCGCGCTTCTCGGCGAGCCCTGAGACCGCGGTGCTGGCGCGCTCAT 420
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Qy 721 ATACCGGGCCAGCAGGGGTGACACCGCGGGCAGTGGCGAAGATGCTGCTGTGGTGTGGT 780
Db 721 ATACCGGGCCAGCAGGGGTGACACCGCGGGCAGTGGCGAAGATGCTGCTGTGGTGTGGT 780
Qy 781 GCTGCTTCTGCTGTACGGACCGACCTATCTGAGCTGGGAGTACTGTGCGGGGGCAG 840
Db 781 GCTGCTTCTGCTGTACGGACCGACCTATCTGAGCTGGGAGTACTGTGCGGGGGCAG 840
Qy 841 CTCATCCCGAGGGCACTGTATGCGAGTTCCTTCTAACAATGCTGCTTCTCATCAC 900
Db 841 CTCATCCCGAGGGCACTGTATGCGAGTTCCTTCTAACAATGCTGCTTCTCATCAC 900
Qy 901 GCTTCTCAACCTGTGAGTTCCTTACGCCCTTCTCAGCGTCACTTCTTAACTCAGCAT 960
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Qy 961 CTACCTGAATCCAGAGCGCACCGCTCCCGGCTGTGATGGGCTCGAGAGCGACCGG 1020
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Qy 1021 CCCGAGCCCTCCCGAGGGCCAGCGCTCAACACCGCCCTGCTGGCTGTGGTGTGGTGTGGT 1080
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Qy 1081 CTGGCAGAGGGGACCGGGAGCGCATGCGCTGCACAGGTATGGGTGGTGGTGGCGC 1140
Db 1081 CTGGCAGAGGGGACCGGGAGCGCATGCGCTGCACAGGTATGGGTGGTGGTGGCGC 1140
Qy 1141 CTTAGCGCTGAGGCGGGGAGCGACCTCCCGGGGTGGCGTGGGGCGGCTCCGTGGC 1200
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Qy 1261 GAGGGGCTCCAGCGCTGGGCTCTCGGCTGCTGGAGAGCGCATGAAGTGGTGTG 1320
Db 1261 GAGGGGCTCCAGCGCTGGGCTCTCGGCTGCTGGAGAGCGCATGAAGTGGTGTG 1320
Qy 1321 CCAGAGCTTCAACAGCGCTTTCGGCTGTCTCGGACAGGAAGTGGCCAGTCCGTGGC 1380
Db 1321 CCAGAGCTTCAACAGCGCTTTCGGCTGTCTCGGACAGGAAGTGGCCAGTCCGTGGC 1380
Qy 1381 CGTCATCGTGAAGCATCTTTGGGCTCTGCTGGGCCCCATACAGCTGTGATCATCCG 1440
Db 1381 CGTCATCGTGAAGCATCTTTGGGCTCTGCTGGGCCCCATACAGCTGTGATCATCCG 1440
Qy 1441 GCGCGCTTCCATGCGCATGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Db 1441 GCGCGCTTCCATGCGCATGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Qy 1501 GTGGGCCAACTCGGCTGTCAACCTGTCTCTACCTCTGTGSCACACAGCTTCCGCGG 1560
Db 1501 GTGGGCCAACTCGGCTGTCAACCTGTCTCTACCTCTGTGSCACACAGCTTCCGCGG 1560
Qy 1561 GGCCTTCAACAGCTGTCTGCCCCAGAGCTCAAAATCCAGCCCGCACAGCTCCCTGGA 1620
Db 1561 GGCCTTCAACAGCTGTCTGCCCCAGAGCTCAAAATCCAGCCCGCACAGCTCCCTGGA 1620
Qy 1621 GCACTGCTGGAAGTGAAGTGGGCCACACAGAGCTTCTCTCAGCCACCGCTCTCTCAGCCCGC 1680
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RESULT 4

US-08-985-090-1

; Sequence 1, Application US/08985090.

Qy 1681 GTCTCTGGGCACTGGCCCTGTCTCCCTTACCCGGCTGTCTCCCTCCAGGGGTGAGCCC 1740
Db 1681 GTCTCTGGGCACTGGCCCTGTCTCCCTTACCCGGCTGTCTCCCTCCAGGGGTGAGCCC 1740
Qy 1741 GCGCGTGTCTGTGGGCTCTCTTAATGACAGGAGACCACTGTCCATGAGAGCGGCTTC 1800
Db 1741 GCGCGTGTCTGTGGGCTCTCTTAATGACAGGAGACCACTGTCCATGAGAGCGGCTTC 1800
Qy 1801 CTGGGTTGGCCAGAGGGCCCTCACTGGCTGACATGGAGGCTGGGTGGCGCCCTGGCC 1860
Db 1801 CTGGGTTGGCCAGAGGGCCCTCACTGGCTGACATGGAGGCTGGGTGGCGCCCTGGCC 1860
Qy 1861 CCCACATTTCTGGCTCCACCGGGAGGAGCTGTGGAGTCCCGACATGCTGCCACCC 1920
Db 1861 CCCACATTTCTGGCTCCACCGGGAGGAGCTGTGGAGTCCCGACATGCTGCCACCC 1920
Qy 1921 CTTGCTGTGGCCACCTTCCGAGTACTGGTGTGTCTTCCAAAGCAAGCACTGG 1980
Db 1921 CTTGCTGTGGCCACCTTCCGAGTACTGGTGTGTCTTCCAAAGCAAGCACTGG 1980
Qy 1981 GTGTCTCCAGGCTTCTGCGCTAGCAGTTTGCCTCTGCAGCTGCACACCTGCACACC 2040
Db 1981 GTGTCTCCAGGCTTCTGCGCTAGCAGTTTGCCTCTGCAGCTGCACACCTGCACACC 2040
Qy 2041 CTTGACACACCTGACACCGCTCTCTCCCGGCAAGCCAGGACACTGCTTTGCTG 2100
Db 2041 CTTGACACACCTGACACCGCTCTCTCCCGGCAAGCCAGGACACTGCTTTGCTG 2100
Qy 2101 CTTGCTGTCTTGTGATAGCTCAGGCTGGCCCTTTCACCCCTTCCCAAGCACTCT 2160
Db 2101 CTTGCTGTCTTGTGATAGCTCAGGCTGGCCCTTTCACCCCTTCCCAAGCACTCT 2160
Qy 2161 CTCTGCCCCAAAAGTGTCAAGGGGCTTAGGAACTCGAAGCTGTCTCTCTCTTTCCA 2220
Db 2161 CTCTGCCCCAAAAGTGTCAAGGGGCTTAGGAACTCGAAGCTGTCTCTCTCTTTCCA 2220
Qy 2221 TTTCTGGGTGTTTTCAGAAAGATGAAGAAACAACTGTCTGTGAATCTGTCTGGG 2280
Db 2221 TTTCTGGGTGTTTTCAGAAAGATGAAGAAACAACTGTCTGTGAATCTGTCTGGG 2280
Qy 2281 ATGTTTAATCAAGAGAGCAAAATTTGTGAGAGCTCAGGGGTGATTTGGCAGGTGGG 2340
Db 2281 ATGTTTAATCAAGAGAGCAAAATTTGTGAGAGCTCAGGGGTGATTTGGCAGGTGGG 2340
Qy 2341 CTCCACGCGCTCTCCCTCCGCTAAGGCTTCCGCTGAGCTGTGCGCAGCTGTCTGCC 2400
Db 2341 CTCCACGCGCTCTCCCTCCGCTAAGGCTTCCGCTGAGCTGTGCGCAGCTGTCTGCC 2400
Qy 2401 CACCCGCGCTCTGGGCTCACACCGCTGTGGGCAAGCCCTGCCCGGCACTCTGTTT 2460
Db 2401 CACCCGCGCTCTGGGCTCACACCGCTGTGGGCAAGCCCTGCCCGGCACTCTGTTT 2460
Qy 2461 GCTCAACAGAGCTCTGGGGTGTGGAGGAGGGGCGCGGTGGCGCCGAGGGTCC 2520
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Qy 2521 CAAAGGCTGCAAGGGGCGGTCCAGAGAGGTGCCCGGAGGGGCGCTTCGSCATGTGCT 2580
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Qy 2581 GTGCACCGCTGCCAGCGCTCTGATGCTCTCTGCTGTGGCGCTGCGCTGCCCTGCA 2640
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Db 2641 AACCGTGAAGTCAAAATGAAGTATTTTTTAAAAAATAAAAAAAAAAAAAAAAAAAAA 2699

; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSES: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
US-08-985-090-1

Query Match 97.6%; Score 2635.2; DB 2; Length 2689;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
QY 25 CGCACCGGCGGCTCAGGCTCCGGCTCCTCTCCGCTGACAGCGCGCTGCCGGCC 84
DB 18 CGCACCGGCGGCTCAGGCTCCGGCTCCTCTCCGCTGACAGCGCGCTGCCGGCC 77
QY 85 CCACCTGGGCTCGATCCGGCCCGCGCCCTCGGCACCGCTGCTGTGGCCCGCGCCG 144
DB 78 CCACCTGGGCTCGATCCGGCCCGCGCCCTCGGCACCGCTGCTGTGGCCCGCGCCG 137
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[illegible]

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RESULT 5
US-09-165-543-1
; Sequence 1, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
US-09-165-543-1

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RESULT 6

US-09-949-016-5059
; Sequence 5059, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5059
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5059

Query Match 97.6%; Score 2633.6; DB 4; Length 2665;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2658; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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Db 7038 ACACGAGCCCTGGTGGCCAAAGCTGCCCCGGCCACTCTGTTTGTCTACCCAGGACCTCTG 7097
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Db 7098 GGGGTTGTTGGAGAGAGGGGCGCGGCTGGGCGCCGAGGGTCCCAAGGCTGCGAGGGCGG 7157
QY 2539 TCCAGAGAGGTGCCCCGGGCGAGGGCGCGCTTCCGCATGTCTGTGACCCGCTGCCACGG 2598
Db 7158 TCCAGAGAGGTGCCCCGGGCGAGGGCGCGCTTCCGCATGTCTGTGACCCGCTGCCACGG 7217
QY 2599 CTCTGCATGCTCTCTGCTGCTGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 2658
Db 7218 CTCTGCATGCTCTCTGCTGCTGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 7277
QY 2659 AAGTGTATTTTTTA 2673
Db 7278 AAGTGTATTTTTTA 7292

RESULT 8
US-09-891-053-13
; Sequence 13, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yuseki
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (293)...(1209)
US-09-891-053-13

Query Match 58.9%; Score 1590.2; DB 4; Length 1893;
Best Local Similarity 98.5%; Pred. No. 1.8e-298;
Matches 1615; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
QY 679 CATCAGCTACGACCGCTTCTGCTCGGTGACCCGAGGGGTCTCATACCGGGCCAGCAGG 738
Db 256 CTTCCGCGCGCGCGCTTGACCGCTTCTGAGGTCTCATACCGGGCCAGCAGG 315


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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 778..2112
; US-09-165-543-4

Query Match
Best Local Similarity 51.3%; Score 1384.8; DB 3; Length 3244;
Matches 2043; Conservative 0; Mismatches 632; Indels 79; Gaps 20;

QY 14 GGCTGACGGTCCGACCGGACGGCTCAGGCTCCGGCTCCTCTCCCGCTGAGCAGCG 73
Db |||
QY 482 GGGTGACCGACGACCGCGGGCGCTGGAGCT-CGGCTTTGCTCTCGCTGAGCAGCG 540
Db |||
QY 74 CGCTGCGGCGCCACTGGGCTGGGA-TCCGGCGCGCGCGCCCTCGGCACGGCT----- 126
Db |||
QY 541 CGCGCGCGCGCCACTCCGCTCAGATTCCGACACACAGCGCCCTCTGGATCGGCCCTCTGG 600
Db |||
QY 127 -----GCTCTGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db |||
QY 601 ACTCTAGCCCGGCTCTTGCTCCGACCCCGCGGACCACTCTCCGGCGCGCGCGCGCGCG 659
Db |||
QY 181 ACCGACCGCGGCAAGGGCCCGCAAGACGAGGCTCCGGCGCGCGCGCGCGCGCGCGCGCG 240
Db |||
QY 660 ACCGGGCTGGCGAGAGCGCGCAAGATTAGGCTCAGCGCGCGCGCGCGCGCGCGCGCGCG 719
Db |||
QY 241 CCCAGTCTCGCGCGCGCGCGCGCTTCCTCGGACGCTGGACCGCGCGCGCGCGCGCGCGCG 300
Db |||
QY 720 CCCAGTCTCCGCGCGCGCGCGCGCGCTTCCTCGGACGCGCTGGAGCGCGCTGGGCGCGCT 779
Db |||
QY 301 GGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db |||
QY 780 GGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 839
Db |||
QY 361 GGCGCGCGCGCGCGCGCGCGCTTCCTCGGACGCTGGACCGCGCGCGCGCGCGCGCGCTCAT 420
Db |||
QY 840 GACTCGAGCGCGCGCGCGCGCGCTTCCTCGGACGCTGGACCGCGCGCGCGCGCGCGCGCTCAT 899
Db |||
QY 421 GGCGTGTCTATGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db |||
QY 900 GGCGTGTCTATGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 959
Db |||
QY 481 CGACTCGAGCTCCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db |||
QY 960 GGATTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1019
Db |||
QY 541 CCTCGTGGCGCGCTTCGTCATCCACTGTATGTACCGCTACGCTGCTGACAGCGCGCTGGAC 600
Db |||
QY 1020 CTTGCGGCGCGCTTCGTCATCCCATTTGATACCGCTATGTGCTGACCGCGCGCTGGAC 1079
Db |||
QY 601 CTTGCGCGCGCGCGCTTCGAACTGTGGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 660
Db |||
QY 1080 CTTGCGCGCGCGCGCTTCGAACTGTGGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 1139
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QY 661 TGGCTTCAACATGTGCTCATCAGCTACGACCGCTTCCTGTGGTGTGGTGTGGTGTGGTGTGG 720
Db |||
QY 1140 GGTCTTCAACATGTGCTCATCAGCTATGACCGATTTCCTGTGAGTGTGGTGTGGTGTGG 1199
Db |||
QY 721 ATACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db |||
QY 1200 CTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1259
Db |||
QY 781 GCTGGCGCTTCCTGTGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db |||
QY 1260 GCTGGCGCTTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1319
Db |||
QY 841 CTCATCCCGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db |||
QY 1320 TTCCATCCCGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1379
Db |||
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2005, 19:57:02 ; Search time 27 Seconds
(without alignments)
1230.327 Million cell updates/sec

Title: US-10-727-021-7
Perfect score: 2361
Sequence: 1 MERAPPDGLNAGALAGDA.....LLCPQKLIKPHSSLEHCWK 445

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2361	100.0	445	3	US-09-167-354-7
2	2361	100.0	445	4	US-09-642-855-7
3	2361	100.0	445	4	US-09-642-514-7
4	2357	99.8	445	2	US-08-985-090-2
5	2357	99.8	445	3	US-09-165-543-2
6	2357	99.8	449	4	US-09-949-016-10930
7	2357	99.8	453	4	US-09-891-053-20
8	2213	93.7	445	3	US-09-165-543-5
9	2213	93.7	445	4	US-09-891-053-25
10	2057	87.1	413	4	US-09-891-053-1
11	1828	77.4	362	2	US-08-985-090-5
12	1828	77.4	362	3	US-09-165-543-32
13	1820	77.1	351	3	US-09-524-162-2
14	724	30.7	390	3	US-09-414-010-2
15	724	30.7	390	4	US-09-812-216-2
16	598.5	25.3	479	1	US-08-313-553-7
17	598.5	25.3	479	3	US-08-767-993-7
18	584.5	24.8	460	4	US-09-826-509-513
19	541	22.9	590	4	US-09-538-092-967
20	540	22.9	355	1	US-08-118-270-11
21	540	22.9	355	5	PCT-US93-08528-11
22	536	22.7	590	4	US-09-826-509-517
23	535	22.7	479	4	US-09-826-509-519
24	527.5	22.3	532	4	US-09-826-509-521
25	527	22.3	348	1	US-08-118-270-13
26	527	22.3	348	5	PCT-US93-08528-13
27	523	22.2	342	1	US-08-118-270-9
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					Sequence 7, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 10930, A
					Sequence 20, Appli
					Sequence 5, Appli
					Sequence 25, Appli
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					Sequence 2, Appli
					Sequence 7, Appli
					Sequence 513, App
					Sequence 967, App
					Sequence 11, Appl
					Sequence 11, Appl
					Sequence 517, App
					Sequence 519, App
					Sequence 521, App
					Sequence 13, Appl
					Sequence 13, Appl
					Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-167-354-7
; Sequence 7, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-167-354-7

Query Match 100.0%; Score 2361; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 3.7e-161;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	ADSSLRQNNFLLNLALSDFLVGAFICPLYPYVYLTGRTWTFGRGLCKLWLVVDLLCTS	120
DB	61	ADSSLRQNNFLLNLALSDFLVGAFICPLYPYVYLTGRTWTFGRGLCKLWLVVDLLCTS	120
QY	121	SAFNIVLSYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG	180
DB	121	SAFNIVLSYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG	180
QY	181	SSIPGHCYAFYFFNYNYFLITASTLEFPTPLSVTFNLSIYLNIORTLRLDGAEEAA	240
DB	181	SSIPGHCYAFYFFNYNYFLITASTLEFPTPLSVTFNLSIYLNIORTLRLDGAEEAA	240
QY	241	GPEPPPEAQPSPPPPPGCGWQKGHEAMPLHRYGVGEAAVGAAGATLGGGGGGSV	300
DB	241	GPEPPPEAQPSPPPPPGCGWQKGHEAMPLHRYGVGEAAVGAAGATLGGGGGGSV	300
QY	301	ASPTSSSGSSRGTERPRSLKRGSKPSASSLEKRMKVQSQSFQTRFLSRDRKVAKSL	360
DB	301	ASPTSSSGSSRGTERPRSLKRGSKPSASSLEKRMKVQSQSFQTRFLSRDRKVAKSL	360

Db 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFSLSDRDKVAKSL 360
QY 361 AVISIFGLCWAPYTLMLIIRAAACHGCVDPDYWTYSFWLLWANSVAVNPVLPCHHSFR 420
Db 361 AVISIFGLCWAPYTLMLIIRAAACHGCVDPDYWTYSFWLLWANSVAVNPVLPCHHSFR 420
QY 421 RAFTKLLCPQKLIKIPHSLSHCWK 445
Db 421 RAFTKLLCPQKLIKIPHSLSHCWK 445

RESULT 2

US-09-642-855-7
; Sequence 7, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,855
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-642-855-7

Query Match 100.0%; Score 2361; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 3.7e-161;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MERAPPDGPLNAGSALAGDAAAAGGARGFSAATVLAALMALLIVATVGLNALVMAFV 60
QY 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
Db 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY 121 SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
Db 121 SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNIOQTRELDCAREAA 240
Db 181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNIOQTRELDCAREAA 240
QY 241 GPEPPEAQSPPPPPGCGWCKQKGHEAMP LHRVGVGEAAVGAAGATLGGGGGGSV 300
Db 241 GPEPPEAQSPPPPPGCGWCKQKGHEAMP LHRVGVGEAAVGAAGATLGGGGGGSV 300
QY 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFSLSDRDKVAKSL 360
Db 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFSLSDRDKVAKSL 360
QY 361 AVISIFGLCWAPYTLMLIIRAAACHGCVDPDYWTYSFWLLWANSVAVNPVLPCHHSFR 420
Db 361 AVISIFGLCWAPYTLMLIIRAAACHGCVDPDYWTYSFWLLWANSVAVNPVLPCHHSFR 420
QY 421 RAFTKLLCPQKLIKIPHSLSHCWK 445
Db 421 RAFTKLLCPQKLIKIPHSLSHCWK 445

RESULT 3

US-09-642-514-7
; Sequence 7, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,514
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-642-514-7

Query Match 100.0%; Score 2361; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 3.7e-161;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
Db 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY 121 SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
Db 121 SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNIOQTRELDCAREAA 240
Db 181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNIOQTRELDCAREAA 240
QY 241 GPEPPEAQSPPPPPGCGWCKQKGHEAMP LHRVGVGEAAVGAAGATLGGGGGGSV 300
Db 241 GPEPPEAQSPPPPPGCGWCKQKGHEAMP LHRVGVGEAAVGAAGATLGGGGGGSV 300
QY 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFSLSDRDKVAKSL 360
Db 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFSLSDRDKVAKSL 360
QY 361 AVISIFGLCWAPYTLMLIIRAAACHGCVDPDYWTYSFWLLWANSVAVNPVLPCHHSFR 420
Db 361 AVISIFGLCWAPYTLMLIIRAAACHGCVDPDYWTYSFWLLWANSVAVNPVLPCHHSFR 420
QY 421 RAFTKLLCPQKLIKIPHSLSHCWK 445
Db 421 RAFTKLLCPQKLIKIPHSLSHCWK 445

RESULT 4

US-08-985-090-2
; Sequence 2, Application US/08985090
; Patent No. 5882893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-090-2

Query Match 99.8%; Score 2357; DB 2; Length 445;
Best Local Similarity 99.8%; Pred. No. 7.2e-161;
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERAPPDGPNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVGLGNALVMLAFV 60
DB 1 MERAPPDGPNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVGLGNALVMLAFV 60
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DB 61 ADSSLRTONNFFLLNLAISDFLVGAFCLPLYVPVYLTGRWTFGRGLCKLWLVVDVLLCTS 120
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DB 121 SAFNIVLISYDRFLSVTRAVSYRAOQDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNLSIYLNTOQRTRLRDLGAREAA 240
DB 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNLSIYLNTOQRTRLRDLGAREAA 240
QY 241 GPEPPEAQSPPPPPGCGWCKQKHGEAMPLHRYGVGEAAVGAAGATLGGGGGGSV 300
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DB 421 RAFTKLLCPQKLIKQPHSSLEHCWK 445

RESULT 5

US-09-165-543-2
; Sequence 2, Application US/09165543
; Patent No. 6093545

GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-165-543-2

Query Match 99.8%; Score 2357; DB 3; Length 445;
Best Local Similarity 99.8%; Pred. No. 7.2e-161;
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERAPPDGPNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVGLGNALVMLAFV 60
DB 1 MERAPPDGPNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVGLGNALVMLAFV 60
QY 61 ADSSLRTONNFFLLNLAISDFLVGAFCLPLYVPVYLTGRWTFGRGLCKLWLVVDVLLCTS 120
DB 61 ADSSLRTONNFFLLNLAISDFLVGAFCLPLYVPVYLTGRWTFGRGLCKLWLVVDVLLCTS 120
QY 121 SAFNIVLISYDRFLSVTRAVSYRAOQDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
DB 121 SAFNIVLISYDRFLSVTRAVSYRAOQDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNLSIYLNTOQRTRLRDLGAREAA 240
DB 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNLSIYLNTOQRTRLRDLGAREAA 240
QY 241 GPEPPEAQSPPPPPGCGWCKQKHGEAMPLHRYGVGEAAVGAAGATLGGGGGGSV 300
DB 241 GPEPPEAQSPPPPPGCGWCKQKHGEAMPLHRYGVGEAAVGAAGATLGGGGGGSV 300
QY 301 ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFSLRDRKVAKSL 360
DB 301 ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFSLRDRKVAKSL 360
QY 361 AVIVSIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFMLWANSVNPVLYPLCHHSFR 420
DB 361 AVIVSIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFMLWANSVNPVLYPLCHHSFR 420
QY 421 RAFTKLLCPQKLIKQPHSSLEHCWK 445
DB 421 RAFTKLLCPQKLIKQPHSSLEHCWK 445

RESULT 6

US-09-949-016-10930
; Sequence 10930, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10930
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10930

Query Match 99.8%; Score 2357; DB 4; Length 449;
Best Local Similarity 99.8%; Pred. No. 7.3e-161;

Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MERAPPDGLNASGALAGDAAAAGARGSAATAVLAALMALLIVATVGLNALVMLAFV	60
DB	5	MERAPPDGLNASGALAGDAAAAGARGSAATAVLAALMALLIVATVGLNALVMLAFV	64
QY	61	ADSSLRTONNFFLLNLAIISDFLVGAFCLPLVYPVYVLTGRWTFGRGLCKLWLVVDVLLCTS	120
DB	65	ADSSLRTONNFFLLNLAIISDFLVGAFCLPLVYPVYVLTGRWTFGRGLCKLWLVVDVLLCTS	124
QY	121	SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG	180
DB	125	SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG	184
QY	181	SSIPGHCYAEFFYNNYFLITASTLEFPTFPLSVTFNLSIYVLTQRTLRDLGAREAA	240
DB	185	SSIPGHCYAEFFYNNYFLITASTLEFPTFPLSVTFNLSIYVLTQRTLRDLGAREAA	244
QY	241	GPEPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV	300
DB	245	GPEPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV	304
QY	301	ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFQRLSRDRKVAKSL	360
DB	305	ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFQRLSRDRKVAKSL	364
QY	361	AVISIFGLCWAPYTLMIIRAACHGCVDPYWTYSFWLLWANSVNPVLPCHHSFR	420
DB	365	AVISIFGLCWAPYTLMIIRAACHGCVDPYWTYSFWLLWANSVNPVLPCHHSFR	424
QY	421	RAFTKLLCPQKIKIOPHSSLEHCWK	445
DB	425	RAFTKLLCPQKIKIOPHSSLEHCWK	449

RESULT 7

US-09-891-053-20
; Sequence 20, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko

; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-053-20

Query Match 99.8%; Score 2357; DB 4; Length 453;
Best Local Similarity 99.8%; Pred. No. 7.3e-161;
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MERAPPDGLNASGALAGDAAAAGARGSAATAVLAALMALLIVATVGLNALVMLAFV	60
DB	1	MERAPPDGLNASGALAGDAAAAGARGSAATAVLAALMALLIVATVGLNALVMLAFV	60
QY	61	ADSSLRTONNFFLLNLAIISDFLVGAFCLPLVYPVYVLTGRWTFGRGLCKLWLVVDVLLCTS	120
DB	61	ADSSLRTONNFFLLNLAIISDFLVGAFCLPLVYPVYVLTGRWTFGRGLCKLWLVVDVLLCTS	120
QY	121	SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG	180
DB	121	SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG	180
QY	181	SSIPGHCYAEFFYNNYFLITASTLEFPTFPLSVTFNLSIYVLTQRTLRDLGAREAA	240
DB	181	SSIPGHCYAEFFYNNYFLITASTLEFPTFPLSVTFNLSIYVLTQRTLRDLGAREAA	240
QY	241	GPEPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV	300
DB	241	GPEPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV	300
QY	301	ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFQRLSRDRKVAKSL	360
DB	301	ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFQRLSRDRKVAKSL	360
QY	361	AVISIFGLCWAPYTLMIIRAACHGCVDPYWTYSFWLLWANSVNPVLPCHHSFR	420
DB	361	AVISIFGLCWAPYTLMIIRAACHGCVDPYWTYSFWLLWANSVNPVLPCHHSFR	420
QY	421	RAFTKLLCPQKIKIOPHSSLEHCWK	445
DB	421	RAFTKLLCPQKIKIOPHSSLEHCWK	445

RESULT 8

US-09-165-543-5
; Sequence 5, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D. J. Goodearl and Sandra Gluckman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/09/165,543
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
Filing DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-165-543-5

Query Match 93.7%; Score 2213; DB 3; Length 445;
Best Local Similarity 93.5%; Pred. No. 1.4e-150;
Matches 417; Conservative 9; Mismatches 18; Indels 2; Gaps 2;
QY 1 MERAPPDGLNASGALAGDAAAGGARGFSAANTAVLAALMALLIVATVGLGNALVWLAFV 60
DB 1 MERAPPDGLNASGALAGDAAAGGARGFSAANTAVLAALMALLIVATVGLGNALVWLAFV 60
QY 61 ADSSLRTQNNFLLNLAISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
DB 61 ADSSLRTQNNFLLNLAISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCAS 120
QY 121 SAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKMLVWLAFLLYGPAILLSWEYLSGG 180
DB 121 SVFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKMLVWLAFLLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNNWFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240
DB 181 SSIPGHCYAEFFYNNWFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGARE-A 239
QY 241 GPEPPPEAQSPPPP-PPGCGWQKQHGEMPLHRYGVGEAAVGAEGEATLGGGGGGGS 299
DB 240 GPEPPPEAQSPPPP-PPGCGWQKQHGEMPLHRYGVGEAGPGVEAGEAALGGGGGGGA 299
QY 300 VASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSTQRPRLSRDRKVKAS 359
DB 300 AASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSTQRPRLSRDRKVKAS 359
QY 360 LAVIVSIFGLCWAPYTLMIIRAACHGCHVDPYWTYETSFLLWANSVNPVLYPLCHHSF 419
DB 360 LAIVSIFGLCWAPYTLMIIRAACHGCHVDPYWTYETSFLLWANSVNPVLYPLCHYSF 419
QY 420 RRAFTKLLCPQKLIKPHSSLEHCWK 445
DB 420 RRAFTKLLCPQKLIKPHGSLEQCWK 445

RESULT 9
US-09-891-053-25
Sequence 25, Application US/09891053
Patent No. 6750322
GENERAL INFORMATION:
APPLICANT: Itadani, Hiraku
APPLICANT: Takimura, Tetsuo
APPLICANT: Nakamura, Takao

APPLICANT: Kobayashi, Masahiko
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Hidaka, Yusuke
APPLICANT: Ohta, Masataka
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
FILE REFERENCE: 06501-083001
CURRENT APPLICATION NUMBER: US/09/891,053
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/JP99/07280
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: PCT/JP98/05967
PRIOR FILING DATE: 1998-12-25
PRIOR APPLICATION NUMBER: JP 11/145661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 445
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-891-053-25

Query Match 93.7%; Score 2213; DB 4; Length 445;
Best Local Similarity 93.5%; Pred. No. 1.4e-150;
Matches 417; Conservative 9; Mismatches 18; Indels 2; Gaps 2;
QY 1 MERAPPDGLNASGALAGDAAAGGARGFSAANTAVLAALMALLIVATVGLGNALVWLAFV 60
DB 1 MERAPPDGLNASGALAGDAAAGGARGFSAANTAVLAALMALLIVATVGLGNALVWLAFV 60
QY 61 ADSSLRTQNNFLLNLAISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
DB 61 ADSSLRTQNNFLLNLAISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCAS 120
QY 121 SAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKMLVWLAFLLYGPAILLSWEYLSGG 180
DB 121 SVFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKMLVWLAFLLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNNWFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240
DB 181 SSIPGHCYAEFFYNNWFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGARE-A 239
QY 241 GPEPPPEAQSPPPP-PPGCGWQKQHGEMPLHRYGVGEAAVGAEGEATLGGGGGGGS 299
DB 240 GPEPPPEAQSPPPP-PPGCGWQKQHGEMPLHRYGVGEAGPGVEAGEAALGGGGGGGA 299
QY 300 VASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSTQRPRLSRDRKVKAS 359
DB 300 AASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSTQRPRLSRDRKVKAS 359
QY 360 LAVIVSIFGLCWAPYTLMIIRAACHGCHVDPYWTYETSFLLWANSVNPVLYPLCHHSF 419
DB 360 LAIVSIFGLCWAPYTLMIIRAACHGCHVDPYWTYETSFLLWANSVNPVLYPLCHYSF 419
QY 420 RRAFTKLLCPQKLIKPHSSLEHCWK 445
DB 420 RRAFTKLLCPQKLIKPHGSLEQCWK 445

RESULT 10
US-09-891-053-1
Sequence 1, Application US/09891053
Patent No. 6750322
GENERAL INFORMATION:
APPLICANT: Itadani, Hiraku
APPLICANT: Takimura, Tetsuo
APPLICANT: Nakamura, Takao
APPLICANT: Kobayashi, Masahiko
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Hidaka, Yusuke
APPLICANT: Ohta, Masataka
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)

```
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1993-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-891-053-1

Query Match      87.1%; Score 2057; DB 4; Length 413;
Best Local Similarity 87.9%; Pred. No. 1.8e-139;
Matches 392; Conservative 8; Mismatches 12; Indels 34; Gaps 3;

QY 1 MERAPPDGLNAGSALAGDAAGGARGSAWTAVALAALMALLIVATVGLGNALVLAFAV 60
Db 1 MERAPPDGLMNASGTLAGEAAGGARGSAWTAVALAALMALLIVATVGLGNALVLAFAV 60
QY 61 ADSSLRTQNNFLLNLAIASDFLVGAFCLPYVPYVLTGRWTFGRGLCKLWLVVDVLLCTS 120
Db 61 ADSSLRTQNNFLLNLAIASDFLVGAFCLPYVPYVLTGRWTFGRGLCKLWLVVDVLLCAS 120
QY 121 SAFNVLISYDFLSVTRAVSYRAQQDTRRAVRKMLVWVLAFLLYGPAILLSWEYLSGG 180
Db 121 SVFNVLISYDFLSVTRAVSYRAQQDTRRAVRKMLVWVLAFLLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCVAEPFYNNYFLITASTLEFFTPFLSVTFNLSIYLNQTRRLDGLDAREAA 240
Db 181 SSIPGHCVAEPFYNNYFLITASTLEFFTPFLSVTFNLSIYLNQTRRLDGLDGRE-A 239
QY 241 GPEPPEAQSPPP-PPGCGCWQKCHGEAMPLHRYGVGEAAVGAEGEATLGGGGGGGS 299
Db 240 GPEPPEAQSPPPPPAPPSCWCPKGGHGEAMPLH----- 273
QY 300 VASPTSSSGSSRGTERPSLRKRGKPSASSASLEKRMKWVSQSFQTRFLSRDRKVKAS 359
Db 274 -----SGSSSSRGTERPSLRKRGKPSASSASLEKRMKWVSQSFQTRFLSRDRKVKAS 327
QY 360 LAVIVSIFGLCWAPYTLMIIRAACHGCHVDPYVYETSFWLLWANSVNPVLYPLCHHSF 419
Db 328 LAIVSIFGLCWAPYTLMIIRAACHGCHVDPYVYETSFWLLWANSVNPVLYPLCHYSF 387
QY 420 RAFTKLLCPQKXKIQPHSLEHCWK 445
Db 388 RFAFTKLLCPQKXKIQPHSLEHCWK 413

RESULT 11
US-08-985-090-5
; Sequence 5, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-985-090-5

Query Match      77.4%; Score 1828; DB 2; Length 362;
Best Local Similarity 92.8%; Pred. No. 3.8e-123;
Matches 337; Conservative 8; Mismatches 16; Indels 2; Gaps 2;

QY 84 GAFCLPYVPYVLTGRWTFGRGLCKLWLVVDVLLCTSSAFNVLISYDFLSVTRAVSYR 143
Db 1 GAFCLPYVPYVLTGRWTFGRGLCKLWLVVDVLLCASSVFNVLISYDFLSVTRAVSYR 60
QY 144 AQGGDTRAVRKMALVWVLAFLLYGPAILLSWEYLSGGSSIPEGHCVAEPFYNNYFLITAS 203
Db 61 AQGGDTRAVRKMALVWVLAFLLYGPAILLSWEYLSGGSSIPEGHCVAEPFYNNYFLITAS 120
QY 204 TLEFFTPFLSVTFNLSIYLNQTRRLDGLDAREAAAGPEPPEAQSPPP-PPGCGCW 262
Db 121 TLEFFTPFLSVTFNLSIYLNQTRRLDGLDGRE-AGPEPPEAQSPPPPPAPPSCWCGW 179
QY 263 QKHGEAMPLHRYGVGEAAVGAEGEATLGGGGGGSVASPTSSSGSSRGTERPSLRK 322
Db 180 PKHGEAMPLHRYGVGEAGPGVEAGEAALGGGGGGGAAASPTSSSGSSRGTERPSLRK 239
QY 323 GSKPSASSASLEKRMKWVSQSFQTRFLSRDRKVKASLAVIVSIFGLCWAPYTLMIIRA 382
Db 240 GSKPSASSASLEKRMKWVSQSFQTRFLSRDRKVKASLAVIVSIFGLCWAPYTLMIIRA 299
QY 383 ACHGCHVDPYVYETSFWLLWANSVNPVLYPLCHHSFRRAFTKLLCPQKXKIQPHSLEH 442
Db 300 ACHGCHVDPYVYETSFWLLWANSVNPVLYPLCHYSFRRAFTKLLCPQKXKIQPHSLEH 359
QY 443 CWK 445
Db 360 CWK 362

RESULT 12
US-09-165-543-32
; Sequence 32, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-165-543-32

Query Match      77.4%; Score 1828; DB 3; Length 362;
Best Local Similarity 92.8%; Pred. No. 3.8e-123;
Matches 337; Conservative 8; Mismatches 16; Indels 2; Gaps 2;

QY 84 GAFCLPYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYR 143
Db 1 GAFCLPYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYR 60
QY 144 AQGGTRAVRKMVLVWVLAFLYPAILSWELSGSSIPGHCVAEFPYNNWYFLITAS 203
Db 61 AQGGTRAVRKMVLVWVLAFLYPAILSWELSGSSIPGHCVAEFPYNNWYFLITAS 120
QY 204 TLEFFTPFLSVTFNLSIYNIQRTLRDLGAREAAAGPEPPPEAQPSPPPP-PPGCGWGCW 262
Db 121 TLEFFTPFLSVTFNLSIYNIQRTLRDLGARE-AGPEPPPPDAQSPSPPPAPPSCWGCW 179
QY 263 QHGHEAMPLHYRGVEAAVGAAGEATLGGGGGGSVASPTSSSGSSSRGTERPRSLKR 322
Db 180 PKHGHEAMPLHYRGVEAGPGVEAGEAALGGGGGGGAAASPTSSSGSSSRGTERPRSLKR 239
QY 323 GSKPSASSASLEKRMKMSQSTQRFRLSRDKVAKSLAVIVSIKLCWAPYTLMIIRA 382
Db 240 GSKPSASSASLEKRMKMSQSTQRFRLSRDKVAKSLAVIVSIKLCWAPYTLMIIRA 299
QY 383 ACHGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFRRAFTKLLCPQKLIKPHSSLEH 442
Db 300 ACHGRCIPDYWYETSFLLWANSVNPVLYPLCHHSFRRAFTKLLCPQKLIKPHSGSLEQ 359
QY 443 CWK 445
Db 360 CWK 362

RESULT 13
US-09-524-162-2
; Sequence 2, Application US/09524162
; Patent No. 6355452
; GENERAL INFORMATION:
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: HUMAN HISTAMINE H3 GENE VARIANT-2
; FILE REFERENCE: GP-70681
; CURRENT APPLICATION NUMBER: US/09/524,162
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
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; ORGANISM: HOMO SAPIENS
; US-09-524-162-2

Query Match      77.1%; Score 1820; DB 3; Length 351;
Best Local Similarity 78.7%; Pred. No. 1.4e-122;
Matches 350; Conservative 1; Mismatches 0; Indels 94; Gaps 2;

QY 1 MERAPPDGPLNASGALAGDAAAAGGARGFSAATVLAALMALLIVATVIGNALVMAFV 60
Db 1 MERAPPDGPLNASGALAGDAAAAGGARGFSAATVLAALMALLIVATVIGNALVMAFV 60
QY 61 ADSSLRTONNPFLLNLAIISDELVGAFCLPYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
Db 61 ADSSLRTONNPFLLNLAIISDFLV-----GRWTFGRGLCKLWLVVDYLLCTS 106
QY 121 SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMVLVWVLAFLYPAILSWELSGS 180
Db 107 SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMVLVWVLAFLYPAILSWELSGS 166
QY 181 SSIPEGHCVAEFPYNNWYFLITASTLEFFTPFLSVTFNLSIYNIQRTLRDLGAREAA 240
Db 167 SSIPEGHCVAEFPYNNWYFLITASTLEFFTPFLSVTFNLSIYNIQRTLRDLGAREAA 226
QY 241 GPEPPPEAQPSPPPPPGCGWCKHGHEAMPLHYRGVEAAVGAAGEATLGGGGGGSV 300
Db 227 GPEPPPEAQPSPPPPPGCGWCKHGHEAMPLH----- 259
QY 301 ASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMSQSTQRFRLSRDKVAKSL 360
Db 260 -----RKVAKSL 266
QY 361 AVISIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFR 420
Db 267 AVISIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFR 326
QY 421 RAFTKLLCPQKLIKPHSSLEHCWK 445
Db 327 RAFTKLLCPQKLIKPHSSLEHCWK 351

RESULT 14
US-09-414-010-2
; Sequence 2, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-414-010-2

Query Match      30.7%; Score 724; DB 3; Length 390;
Best Local Similarity 38.6%; Pred. No. 3.3e-44;
Matches 164; Conservative 56; Mismatches 131; Indels 74; Gaps 10;

QY 30 SAAWTAVLAALMALLIVATVIGNALVMAFVADSSLRTONNPFLLNLAIISDFVGAFCIP 89
Db 11 SLSTRVTLAFAFMSLVAFALMIGNALVILAFVVDKRLHRSSYFFFLNLAIISDFVGVISIP 70
QY 90 LYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAQQGDT 149
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Db 71 LYIPHTLP-EMDFGKEICVFWLTDDYLLCTASVNIHVLISYDRYLSVNAVSYRQHTGV 129
QY 150 RRAVRKMLLVWVLAFLLYGPAIL---SWEYLSGGSSIPEG-HCYAEFFVNNYFLITASTL 205
Db 130 LKIVTLMAVWVLAFLVNGPMLVSESWK-----DEGSECEPGFFSEWILAITSF 181
QY 206 BEFTFPLSVTFPFLNLSIYLNIOQRTRLRDGAREAGPEPPPAQSPPPPCWGCWQKG 265
Db 182 EVVIPVILVAYFNMIY-----WSLWKRD 205
QY 266 HGEAMPLHRYGVGEAAVGAEEATLGGGGGGSVASPTSSSGSS-----SRGTERPR 318
Db 206 HLSRCQSH-----PGLTAVSSNICGHSFGRLLSSRRSLASASTEVPAFHSERQRKS 257
QY 319 SLKRGSKPSASASLEKRMKMWVSQFT-----QRFRLSRDRKVAKSLAVIVSIFGLCWA 372
Db 258 SLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRARRLAKSLAILLGVFAVCWA 317
QY 373 PYTLLMIIRAAACHGCHVP-DYHYETSFWLLWANSVNPVLYPLCHHSFRRAFTKLLCPQK 431
Db 318 PYSLFTIIVLSFYSSATGPKSVMYRIAFWLFQWNSFVNPLLYPLCHKRFQKAPLKIFC--- 374
QY 432 LKIQP 436
Db 375 IKQOP 379

RESULT 15

US-09-812-216-2
; Sequence 2, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2

Query Match 30.7%; Score 724; DB 4; Length 390;
Best Local Similarity 38.6%; Pred. No. 3.3e-44;
Matches 164; Conservative 56; Mismatches 131; Indels 74; Gaps 10;
QY 30 SAAWTAVALAALMALIVATVLGNALVLAFAVDASLRTQNNFFLNLAISDFLVGAFQIP 89
Db 11 SLSTRVTLAFLMSLVAFALMUGNALVILAFVVDKLRHRSYFFLNLAISDFLVGVSIP 70
QY 90 LYVPVLTGRWTFGRGLCKLMLVVDYLLCTSAFNLVLSYDRFLSVTRAVSYRAQQGDT 149
Db 71 LYIPHTLP-EMDFGKEICVFWLTDDYLLCTASVNIHVLISYDRYLSVNAVSYRQHTGV 129
QY 150 RRAVRKMLLVWVLAFLLYGPAIL---SWEYLSGGSSIPEG-HCYAEFFVNNYFLITASTL 205
Db 130 LKIVTLMAVWVLAFLVNGPMLVSESWK-----DEGSECEPGFFSEWILAITSF 181
QY 206 BEFTFPLSVTFPFLNLSIYLNIOQRTRLRDGAREAGPEPPPAQSPPPPCWGCWQKG 265
Db 182 EVVIPVILVAYFNMIY-----WSLWKRD 205

QY 266 HGEAMPLHRYGVGEAAVGAEEATLGGGGGGSVASPTSSSGSS-----SRGTERPR 318
Db 206 HLSRCQSH-----PGLTAVSSNICGHSFGRLLSSRRSLASASTEVPAFHSERQRKS 257
QY 319 SLKRGSKPSASASLEKRMKMWVSQFT-----QRFRLSRDRKVAKSLAVIVSIFGLCWA 372
Db 258 SLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRARRLAKSLAILLGVFAVCWA 317
QY 373 PYTLLMIIRAAACHGCHVP-DYHYETSFWLLWANSVNPVLYPLCHHSFRRAFTKLLCPQK 431
Db 318 PYSLFTIIVLSFYSSATGPKSVMYRIAFWLFQWNSFVNPLLYPLCHKRFQKAPLKIFC--- 374
QY 432 LKIQP 436
Db 375 IKQOP 379

Search completed: June 2, 2005, 20:41:49
Job time : 29 secs